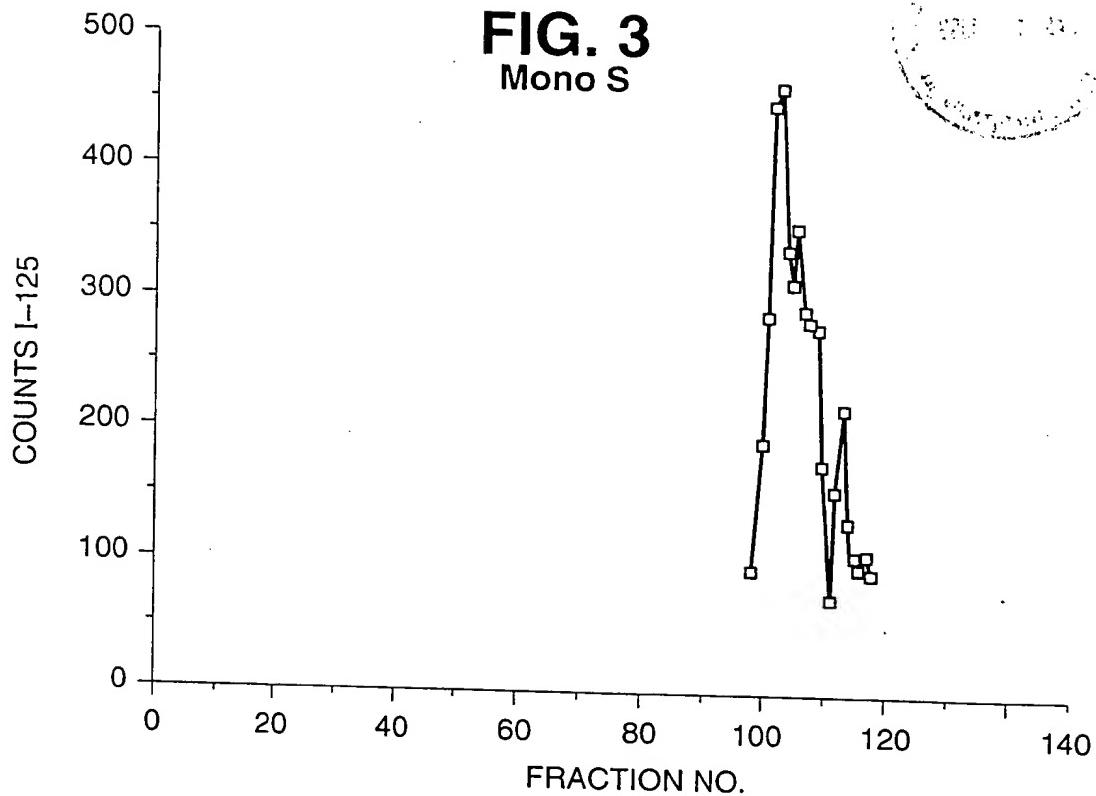
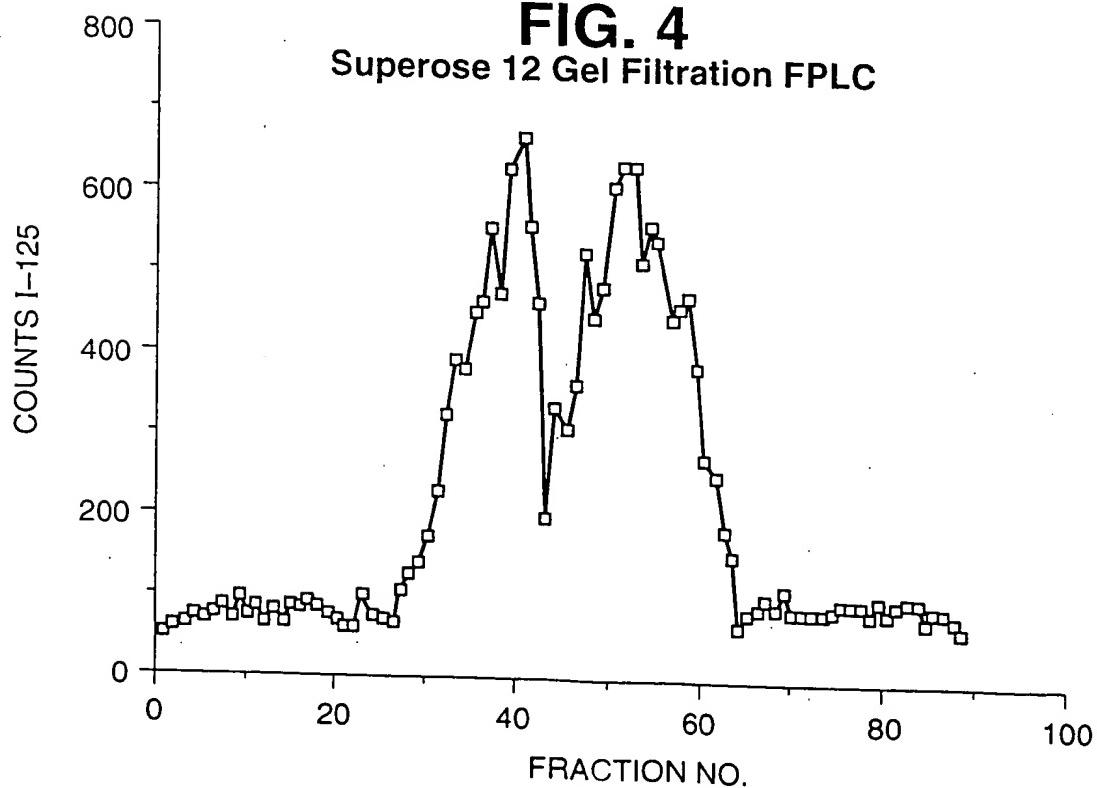


**FIG. 3**  
Mono S



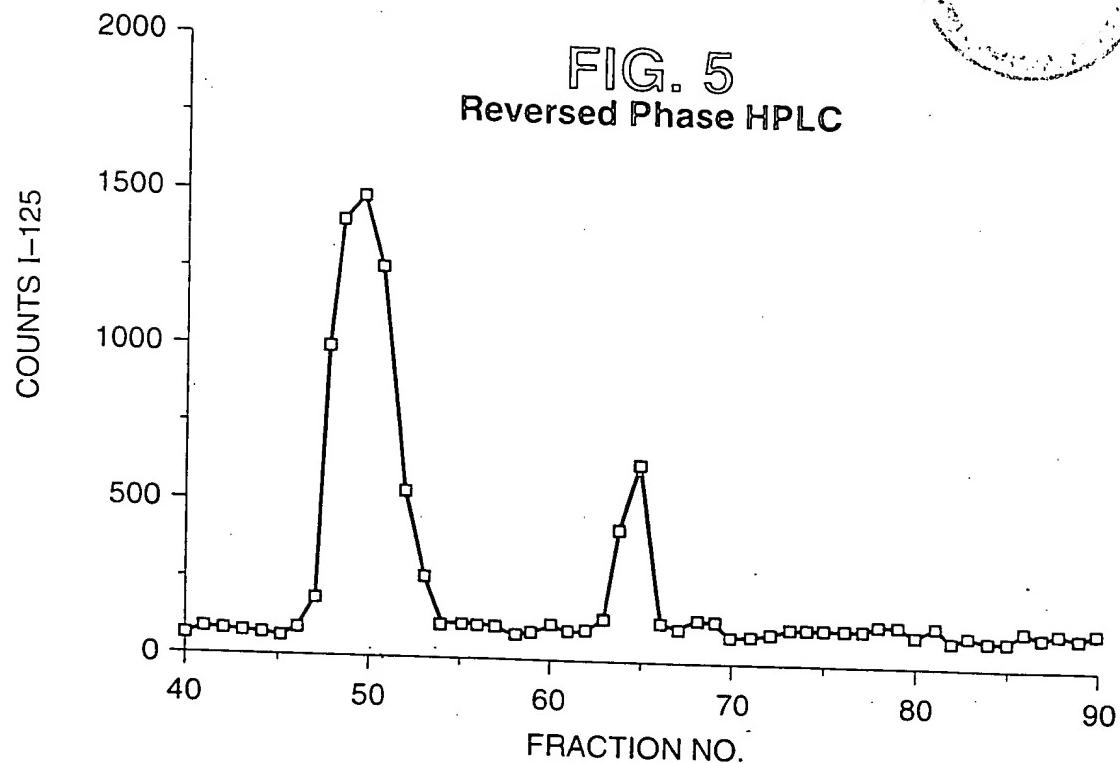
**FIG. 4**  
Superose 12 Gel Filtration FPLC



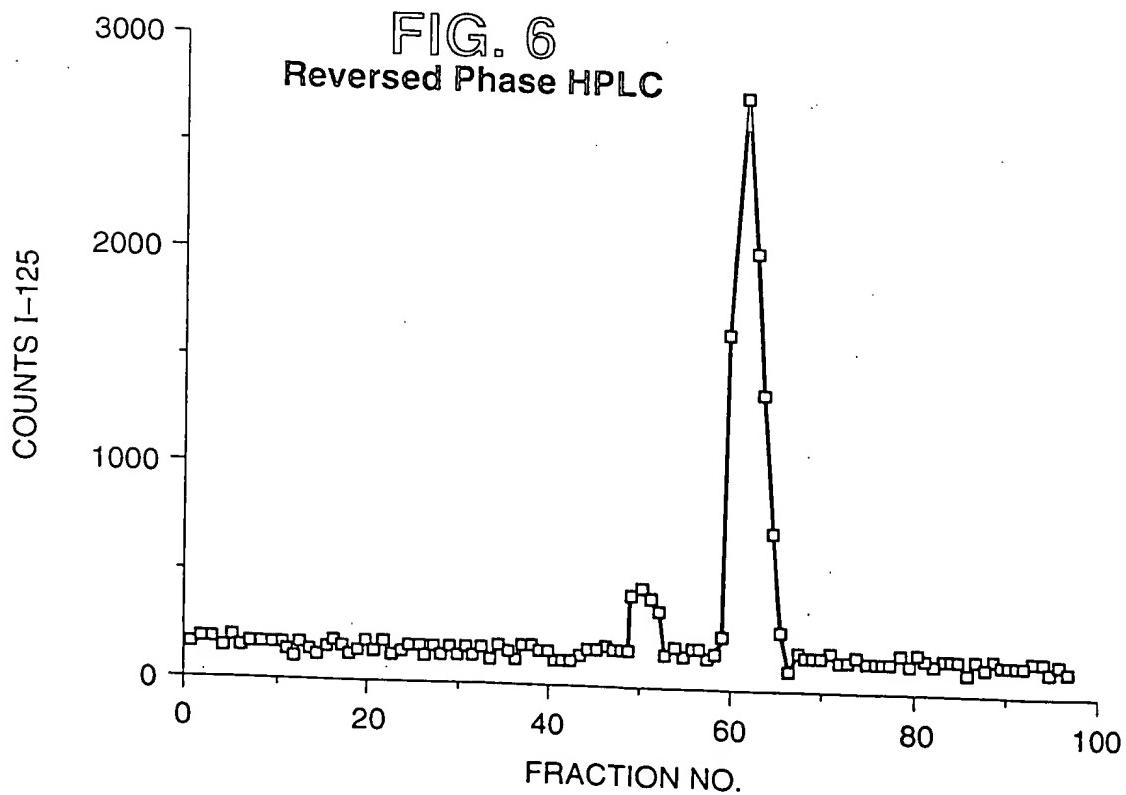
3/78

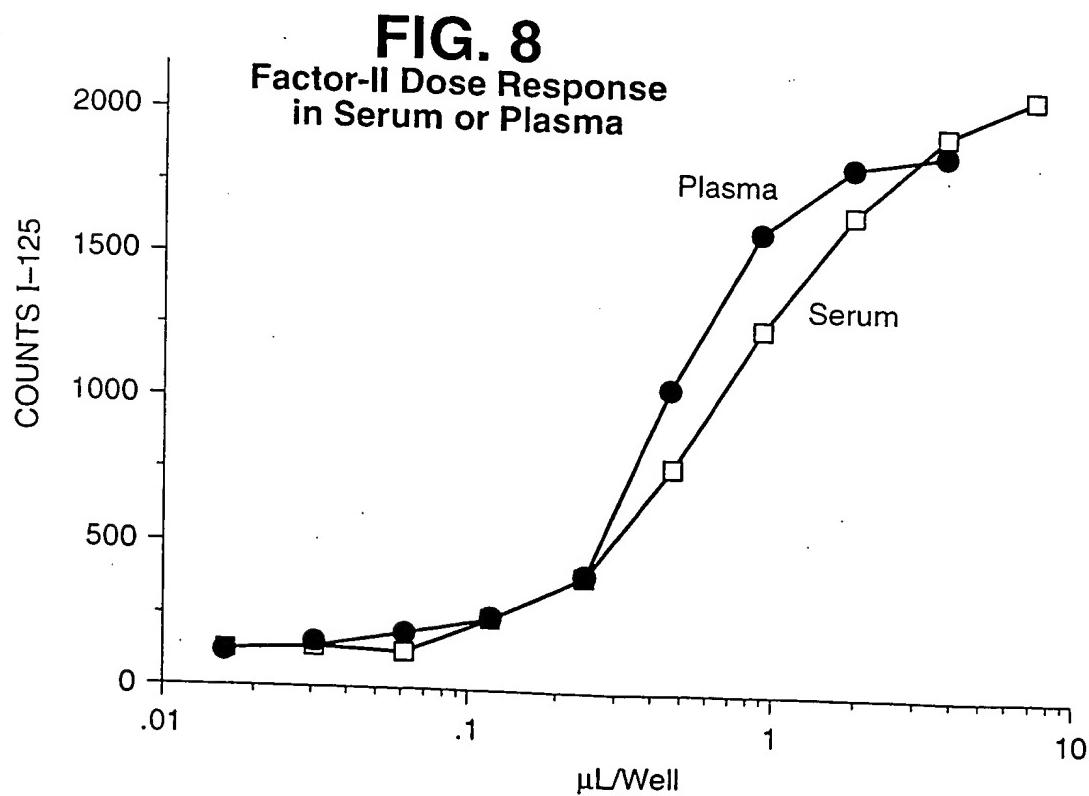
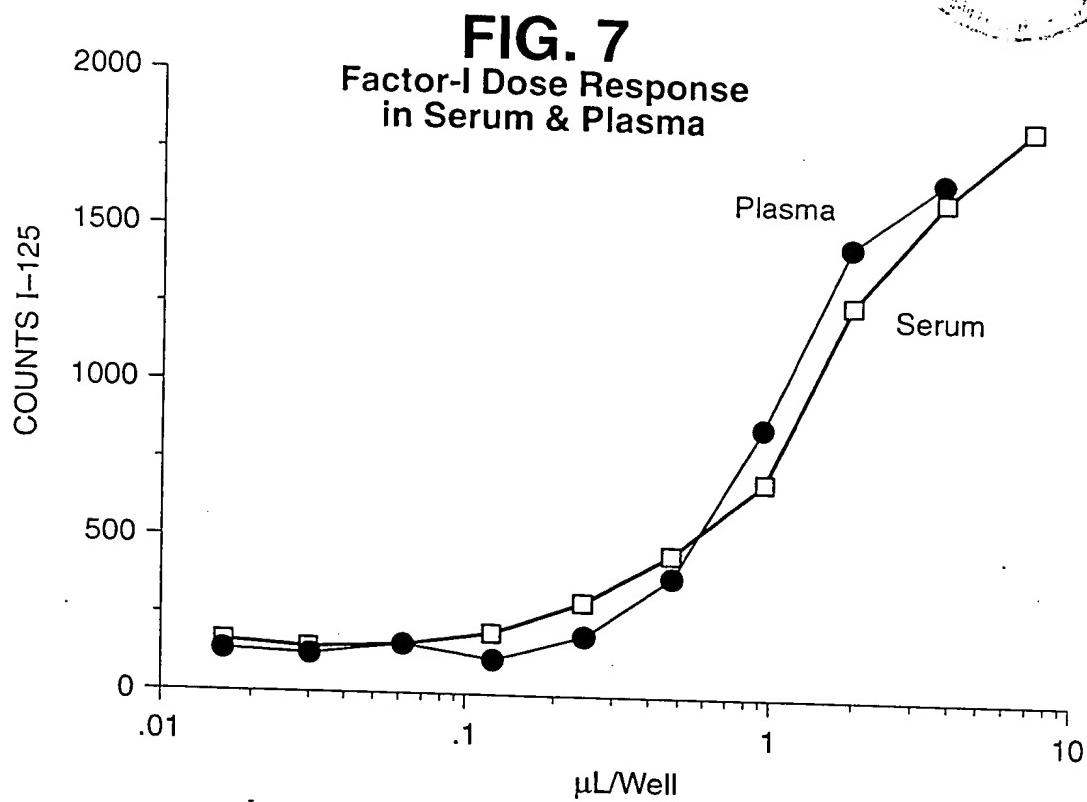


**FIG. 5**  
Reversed Phase HPLC



**FIG. 6**  
Reversed Phase HPLC





# FIG. 9

N-terminus  
GGF-I 01 F K G D A H T E

## Trypsin peptides

GGF-I 02	K/R A S L A D E Y E Y M X K *	(SEQ ID NO: 2)
GGF-I 03	K/R T E T S S S G L X L K *	(SEQ ID NO: 3)
GGF-I 04	K/R K L G E N W A E	(SEQ ID NO: 4)
GGF-I 05	K/R L G E K R A	(SEQ ID NO: 5)
GGF-I 06	K/R I K S E H A G L S I G D T A K *	HMG-1?
GGF-I 07	K/R A S L A D E Y E Y M R K *	HMG-2
GGF-I 08	K/R I K G E H P G L S I G D V A K *	(SEQ ID NO: 6)
GGF-I 09	K/R M S E Y A F F V Q T X R *	(SEQ ID NO: 7)
GGF-I 10	K/R S E H P G L S I G D T A K *	(SEQ ID NO: 8)
GGF-I 11	K/R A G Y F A E X A R *	HMG-1
GGF-I 12	K/R K L E F L X A K *	(SEQ ID NO: 9)
GGF-I 13	K/R T T E M A S E Q G A	HMG-2
GGF-I 14	K/R A K E A L A A L K *	(SEQ ID NO: 10)
GGF-I 15	K/R F V L Q A K K *	HMG-1
GGF-I 16	K/R L G E M W	(SEQ ID NO: 11)
		(SEQ ID NO: 12)
		(SEQ ID NO: 13)
		(SEQ ID NO: 14)
		(SEQ ID NO: 15)
		(SEQ ID NO: 16)
		HMG-1

## Protease V8 peptides

GGF-I 17	E T Q P D P G Q I L K K V P M V I G A Y T	(SEQ ID NO: 169)
GGF-I 18	E Y K C L K F K W F K K A T V M	(SEQ ID NO: 17)
GGF-I 19	E A K Y F S K X D A	(SEQ ID NO: 18)
GGF-I 20	E X K F Y V P	(SEQ ID NO: 19)
GGF-I 21	E L S F A S V R L P G C P P G V D P M V S F P V A L	(SEQ ID NO: 20)

LH-alpha  

 LH-beta

10-A

FIG. 10  
10 A

GGF-I 01 F K G D A H T E  
GGF-I 02 A S L A D E Y E Y M X K  
GGF-I 03 T E T S S S G L X L K  
GGF-I 07 A S L A D E Y E Y M R K  
GGF-I 11 A G Y F A E X A R  
GGF-I 13 T T E M A S E Q G A  
GGF-I 14 A K E A L A A L K  
GGF-I 15 F V L Q A K K  
GGF-I 17 E T Q P D P G Q I L K K V P M V I G A Y T  
GGF-I 18 E Y K C L K F K W F K K A T V M  
(SEQ ID NO: 1)  
(SEQ ID NO: 22)  
(SEQ ID NO: 23)  
(SEQ ID NO: 24)  
(SEQ ID NO: 25)  
(SEQ ID NO: 26)  
(SEQ ID NO: 27)  
(SEQ ID NO: 28)  
(SEQ ID NO: 29)  
(SEQ ID NO: 17)

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10-B

GGF-I 20 E X K F Y V P  
GGF-I 12 K L E F L X A K  
(SEQ ID NO: 19)  
(SEQ ID NO: 32)

# FIG. 11

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Trypsin peptides	
GGF-II 01	K/R V H Q V W A A K *
GGF-II 02	K/R Y I F F M E P E A X S S G
GGF-II 03	K/R L G A W G P P A F P V X Y
GGF-II 04	K/R W F V V I E G K *
GGF-II 05	K/R A L A A A G Y D V E K *
GGF-II 06	K/R L V L R *
GGF-II 07	K/R X X Y P G Q I T S N
GGF-II 08	K/R A S P V S V G S V Q E L V Q R *
GGF-II 09	K/R V C L L T V A A P P T
GGF-II 10	K/R D L L L X V
Histone H1	
GGF-II 11	(SEQ ID NO: 33)
GGF-II 12	(SEQ ID NO: 34)
	(SEQ ID NO: 35)
	(SEQ ID NO: 36)
	(SEQ ID NO: 164)
	(SEQ ID NO: 165)
	(SEQ ID NO: 166)
	(SEQ ID NO: 37)
	(SEQ ID NO: 38)
	(SEQ ID NO: 39)
Lysyl Endopeptidase-C peptides	
GGF-II 11	K V H Q V W A A K *
GGF-II 12	K A S L A D S G E Y M X K *
	(SEQ ID NO: 51)
	(SEQ ID NO: 52)

# FIG. 12

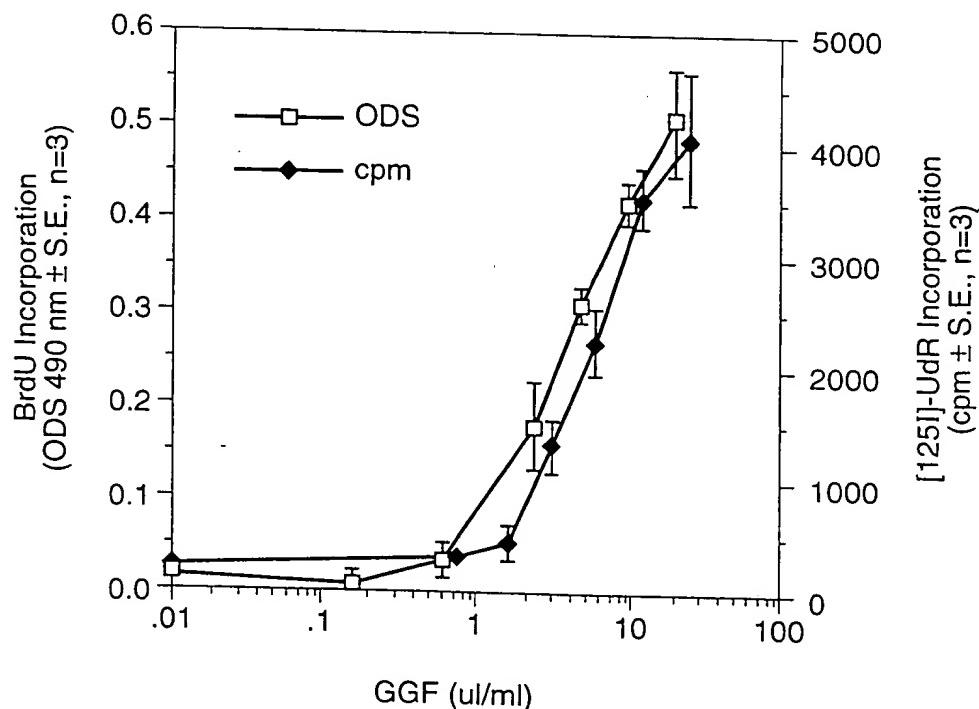
A

GGF-II 01	V H Q V W A A K	(SEQ ID NO: 45)
GGF-II 02	Y I F F M E P E A X S S G	(SEQ ID NO: 46)
GGF-II 03	L G A W G P P A F P V X Y	(SEQ ID NO: 47)
GGF-II 04	W F V V I E G K	(SEQ ID NO: 48)
GGF-II 08	A S P V S V G S V Q E L V Q R	(SEQ ID NO: 49)
GGF-II 09	V C L L T V A A P P T	(SEQ ID NO: 50)
GGF-II 11	K V H Q V W A A K	(SEQ ID NO: 51)
GGF-II 12	K A S L A D S G E Y M X K	(SEQ ID NO: 52)

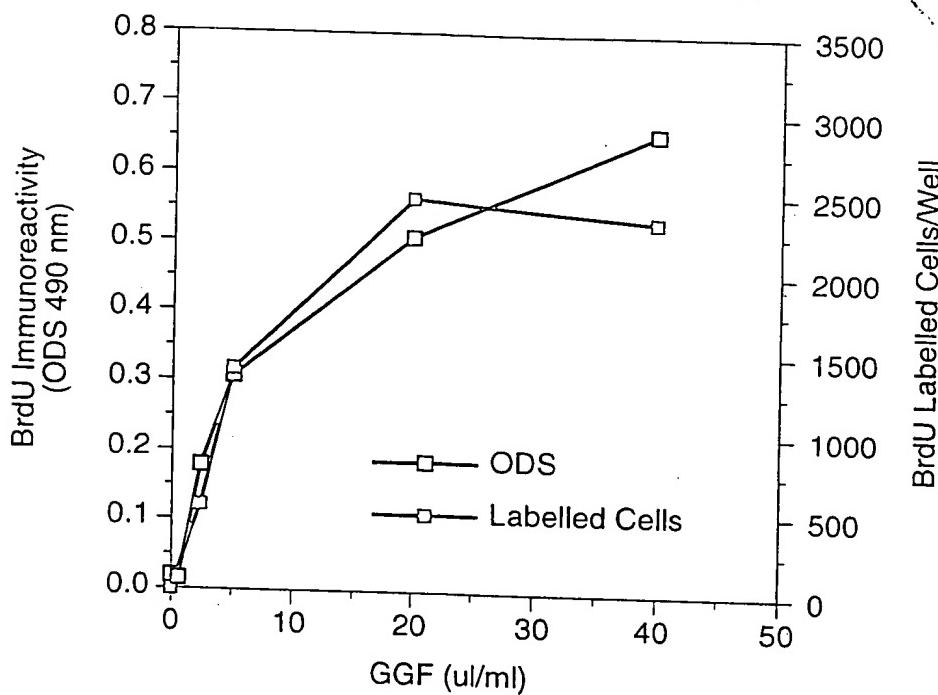
B Novel Factor II Peptides - others

GGF-II 10	D L L L X V	(SEQ ID NO: 53)
-----------	-------------	-----------------

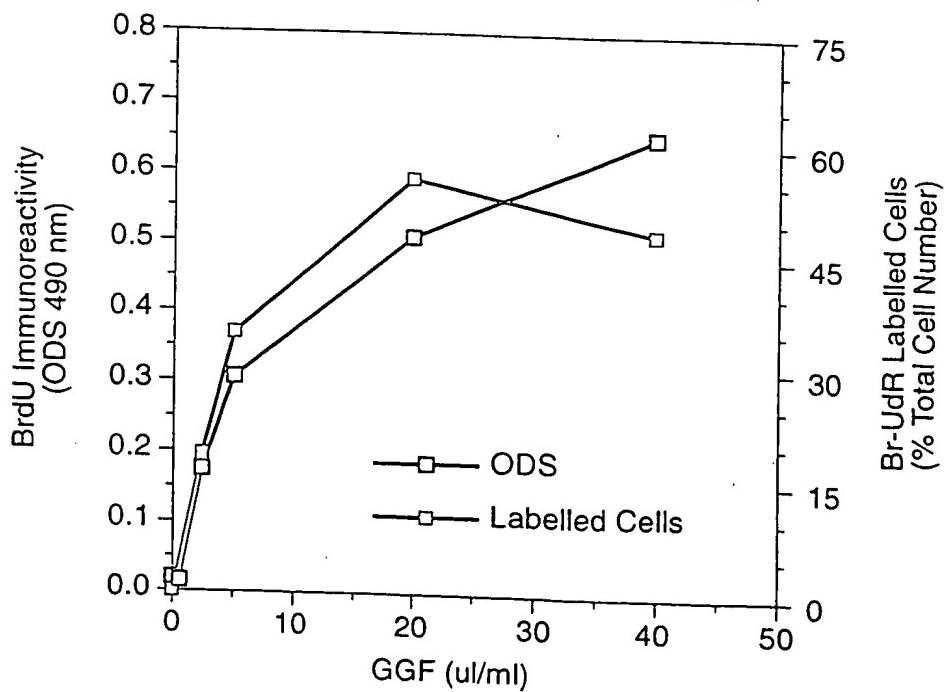
**FIG. 13**  
Comparison of BrdU-ELISA and [<sup>125</sup>I]UdR Counting Method for  
the DNA Synthesis Assay in Schwann Cell Cultures



**FIG. 14A**  
**Comparison of Br-UdR Immunoreactivity  
 and Br-UdR Labelled Cell Number**



**FIG. 14B**  
**Comparison of Br-UdR Immunoreactivity  
 and Br-UdR Labelled Cell Number**



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FIG. 15  
Mitogenic Response of Rat Sciatic Nerve Schwann cell to GGFs

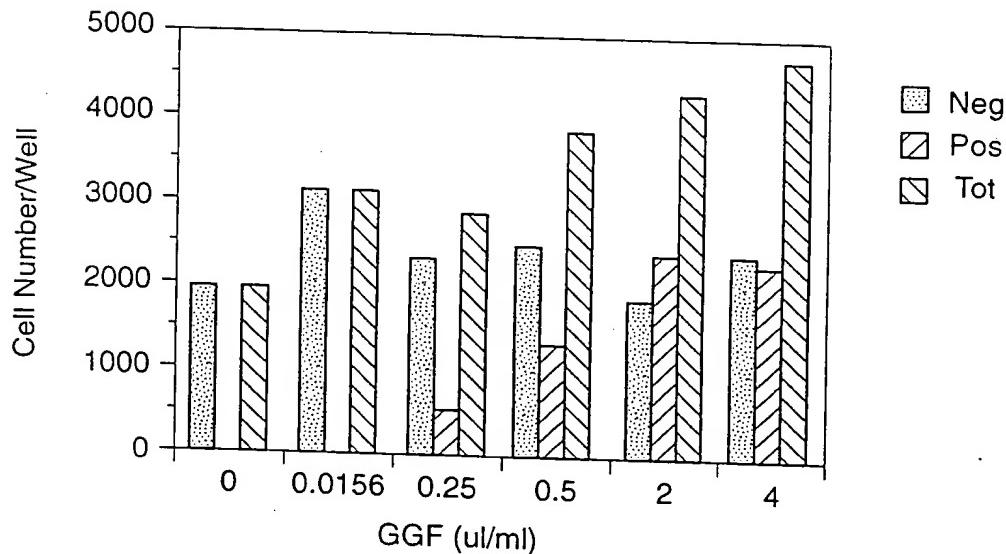
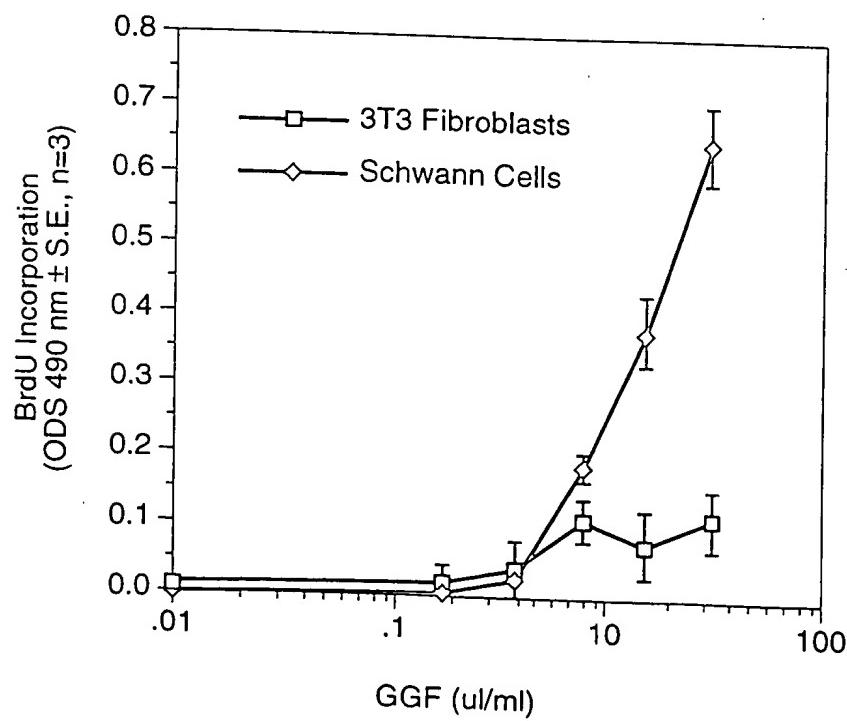
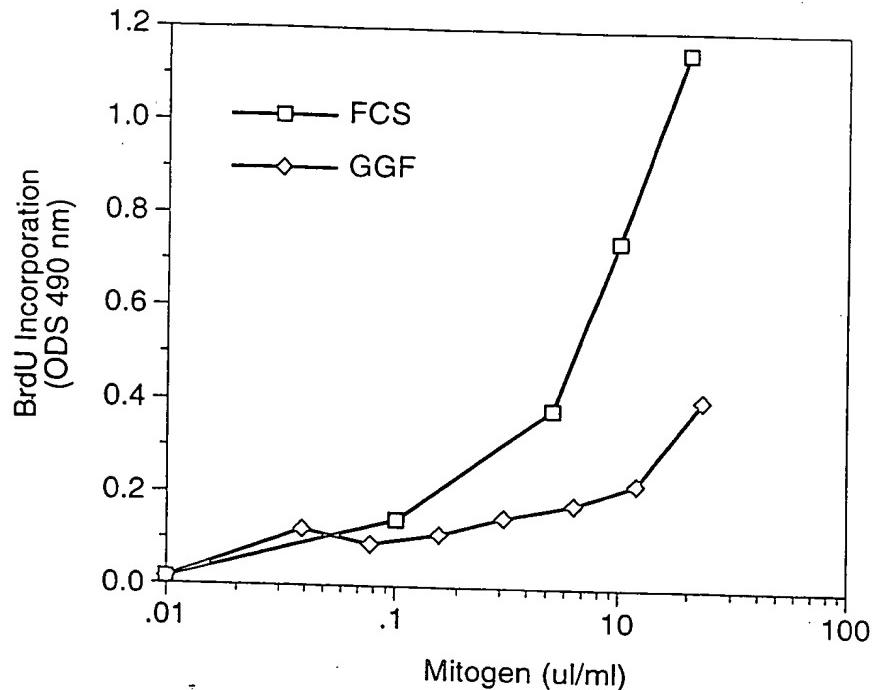


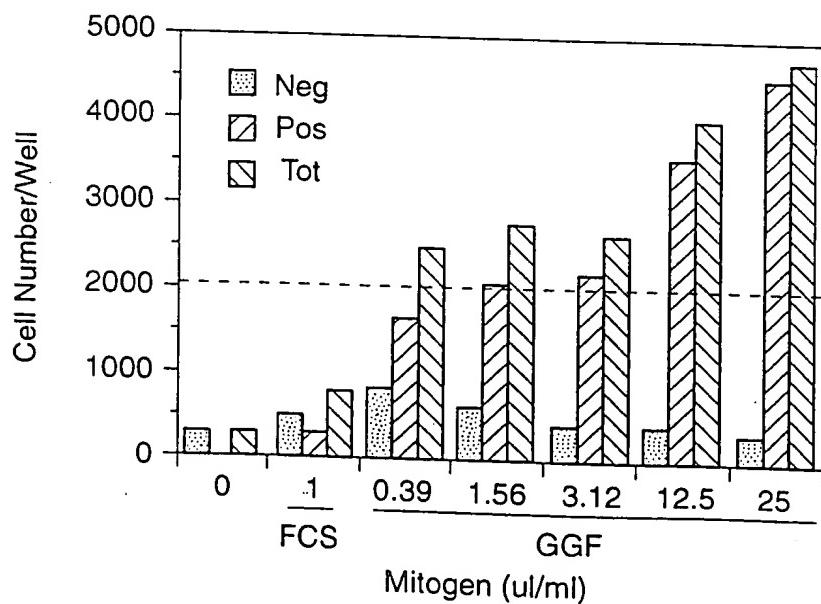
FIG. 16  
DNA Synthesis in Rat Sciatic Nerve Schwann Cells and 3T3 Fibroblasts in the presence of GGFs



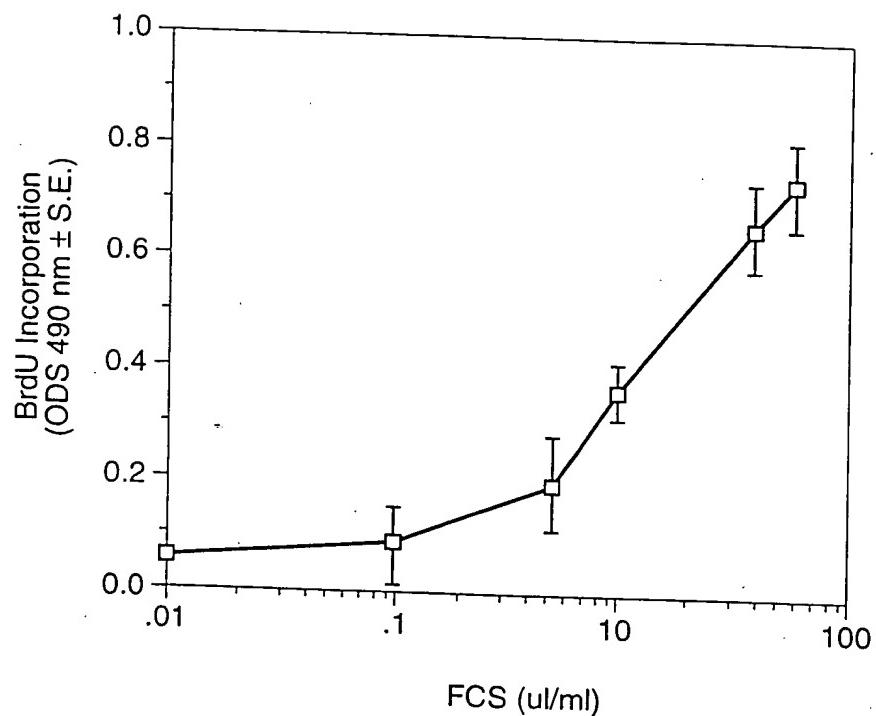
**FIG. 17**  
**Mitogenic Response of**  
**BHK 21 C13 Cells to FCS and GGFs**



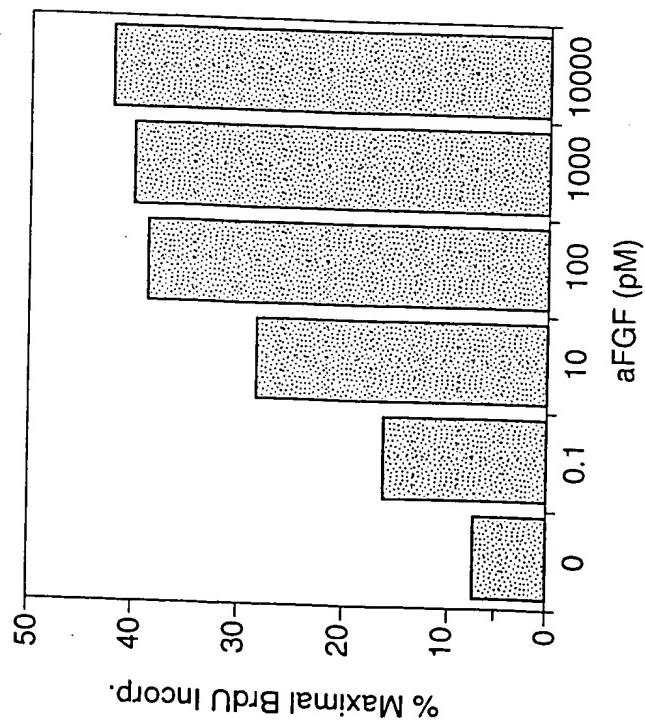
**FIG. 18**  
**Survival and Proliferation of BHK21 C13 Cell**  
**Microcultures After 48 Hours in Presence of GGFs**



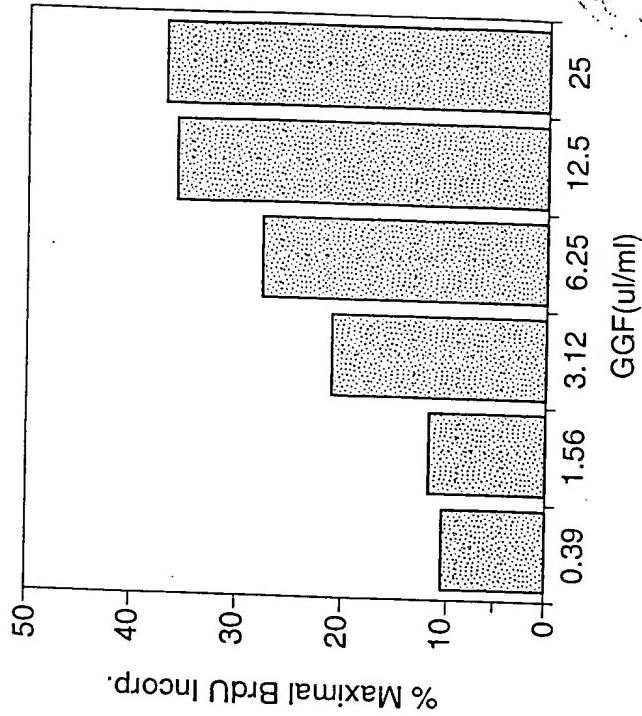
**FIG. 19**  
Mitogenic Response  
of C6 Cells to FCS



**FIG. 20A**  
Mitogenic Response of  
C6 Cells to aFGF & GGFs



**FIG. 20B**  
Mitogenic Response of  
C6 Cells to aFGF & GGFs





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**FIG. 21**  
**Degenerate Oligonucleotide Probes for Factor I & Factor II**

Oligo	Sequence	Peptide	
535	TTYAARGGNGAYGCNCAYAC!	GGFI-1	(SEQ ID NO: 54)
536	CATRTAYTCRTAYTCRTCNGC!	GGFI-2	(SEQ ID NO: 55)
537	TGYTCNGANGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 56)
538	TGYTCRCTNGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 57)
539	CCDATNACCATNGGNACYTT!	GGFI-17	(SEQ ID NO: 58)
540	GCNGCCCANACYTGRTGNAC!	GGFII-1	(SEQ ID NO: 59)
541	GCYTCNGGYTCCATRAARAA!	GGFII-2	(SEQ ID NO: 60)
542	CCYTCDATNACNACRAACCA!	GGFII-4	(SEQ ID NO: 61)
543	TCNGCRAARTANCCNGC!	GGFI-11	(SEQ ID NO: 62)
544	GCNGCNAGNGCYTCYTNGC!	GGFI-14	(SEQ ID NO: 63)
545	GCNGCYAANGCYTCYTNGC!	GGFI-14	(SEQ ID NO: 64)
546	TTYTTNGCYTGNAGNACRAA!	GGFI-15	(SEQ ID NO: 65)
551	TTYTTNGCYTGYAANACRAA!	GGFI-15	(SEQ ID NO: 66)
568	TGNACNAGYTCYTGNAC!	GGFII-8	(SEQ ID NO: 67)
569	TGNACYAAYTCYTGNAC!	GGFII-8	(SEQ ID NO: 68)
609	CATRTAYTCNCCNGARTCNGC!	GGFII-12	(SEQ ID NO: 69)
610	CATRTAYTCNCCRCTRTCNGC!	GGFII-12	(SEQ ID NO: 70)
649	NGARTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 71)
650	NGARTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 72)
651	RCTRTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 73)
652	RCTRTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 74)
653	NGARTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 75)
654	NGARTCNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 76)
655	RCTRTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 77)
656	RCTRCTNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 78)
659	ACNACNGARATGGCTNNGA!	GGFI-13	(SEQ ID NO: 79)
660	ACNACNGARATGGCAGYNGA!	GGFI-13	(SEQ ID NO: 80)
661	CAYCARGTNTGGGNGCNAA!	GGFII-1	(SEQ ID NO: 81)
662	TTYGTNGTNATHGARGGNAA!	GGFII-4	(SEQ ID NO: 82)
663	AARGGNGAYGCNCAYACNGA!	GGFI-1	(SEQ ID NO: 83)
664	GARGCNYTNGCNGCNYTNAA!	GGDI-14	(SEQ ID NO: 84)
665	GTNGGNTCNGTNCARGARYT!	GGFII-8	(SEQ ID NO: 85)
666	GTNGGNAGYGTNCARGARYT!	GGFII-8	(SEQ ID NO: 86)
694	NACYTTYTTNARHATYTGNC!	GGFI-17	(SEQ ID NO: 87)
			(SEQ ID NO: 88)

**FIG. 22**  
**Putative Bovine Factor II Gene Sequences**

SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Val Leu Xaa Asn Ile	53
CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile	101
AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile	149
AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu	197
TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg	245
GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu	293
ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu	341
AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA Lys Tyr Leu Met GLY Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu	389
ATA GAC CTG AAA TAT ATA TAG ATT ATT T Ile Asp Leu Lys Tyr Ile Xaa Ile Ile	417

Degenerate PCR Primers	Oligo Sequence	Peptide
657	CCGAATTCTGCAGGARAACNCARCCNGAYCCNGG!	GGFI-17 (SEQ ID NO: 90)
658	AAGGATCCTGCAGGNTRTANTCNCCHATNACCATNGG!	GGFI-17 (SEQ ID NO: 91)
667	CCGAATTCTGCAGGCNGAYTCNGNGARTAYATG!	GGFI-12 (SEQ ID NO: 92)
668	CCGAATTCTGCAGGCNGAYATYGGNGARTAYAT!	GGFI-12 (SEQ ID NO: 93)
669	AAGGATCCTGCAGNNNCATRRTAYTCNCNGARTC!	GGFII-12 (SEQ ID NO: 94)
670	AAGGATCCTGCAGGNNCATRRTAYTCNCRRRTTC!	GGFII-12 (SEQ ID NO: 95)
671	CCGAATTCTGCAGCAYCARGTNTGGCNGCNAA!	GGFII-1 (SEQ ID NO: 96)
672	CCGAATTCTGCAGATRTTYATGGARCCNGARG!	GGFII-2 (SEQ ID NO: 97)
673	CCGAATTCTGCAGGGGNCCNCNIGCNTTYCCNGT!	GGFII-3 (SEQ ID NO: 98)
674	CCGAATTCTGCAGACTGGTTYGTNGTNATHGARGG!	GGFII-4 (SEQ ID NO: 99)
677	AAGGATCCTGCAGCAGYTNGCNGCCCANACYTGRTG!	GGFII-1 (SEQ ID NO: 100)
678	AAGGATCCTGCAGGYTTCAGYTTCATRAARAA!	GGFII-2 (SEQ ID NO: 101)
679	AAGGATCCTGCAGACNGGRAANGCNGGGNCC!	GGFII-3 (SEQ ID NO: 102)
680	AAGGATCCTGCAGYTTNCYC DATNACNAACRAAC!	GGFII-4 (SEQ ID NO: 103)
681	CATRTAYTCRTAYTCTCNGCAAGGATCCTGCAG!	GGFI-2 (SEQ ID NO: 104)
682	CCGAATTCTGCAGAARGGNGAYGCNCAYACNGA!	GGFI-1 (SEQ ID NO: 105)
683	GCNGCYAANGCYRCYTTNGCAAGGATCCTGCAG!	GGFI-14 (SEQ ID NO: 106)
684	GCNGCNAGNGCYTCYTTNGCAAGGATCCTGCAG!	GGFI-14 (SEQ ID NO: 107)
685	TCNGCRAARTANCNGCAAGGATCCTGCAG!	GGFII-1 (SEQ ID NO: 108)

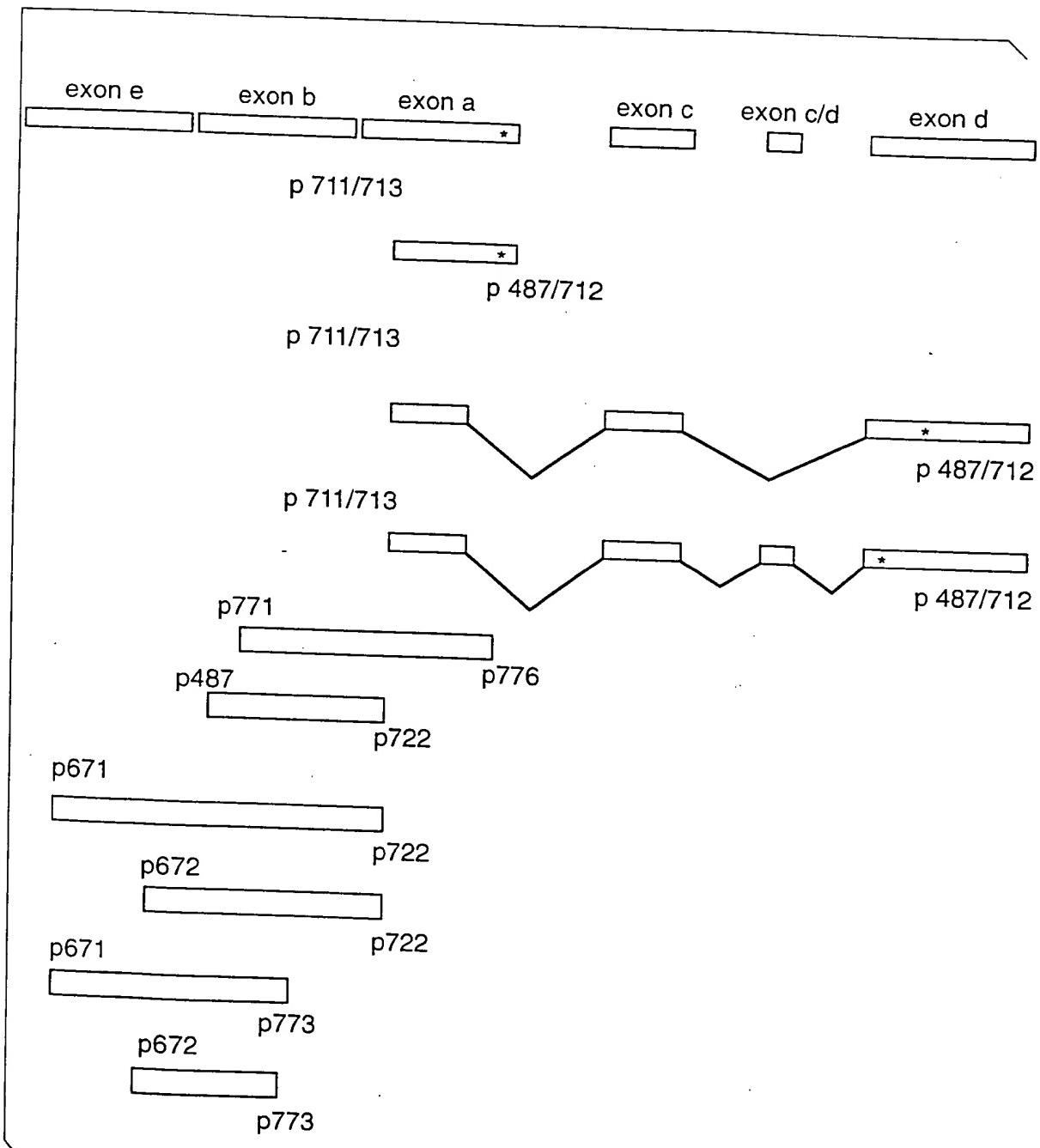
FIG. 23A  
PCR Primers for Factor I & Factor II

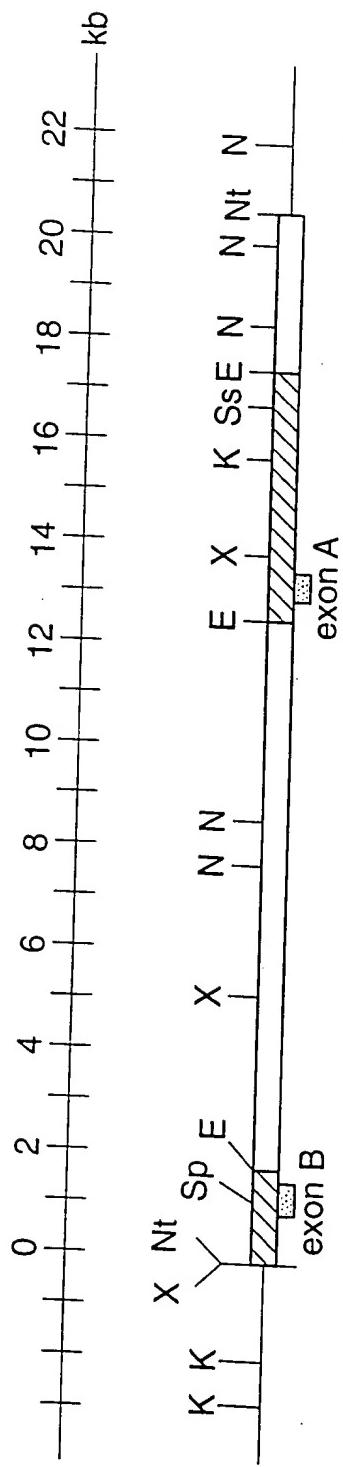
Oligo	Sequence	Comment
711	CATCGATCTGCAGGCTGATTCTGGAGAATATATGTGCA!	3' RACE
712	AAGGATCCTGCAGCCACATCTCGAGTCGACATCGATT!	3' RACE
713	CCGAATTCTGCAGTGTGATCAGCAAACTAGGAAATGACA!	3' RACE
721	CATCGATCTGCAGCTAGTTTGCTGATCACTTTGCAC!	5' RACE
722	AAGGATCCTGCAGTATATTCTCCAGAACATAGCCAGTG!	5' RACE; ANCHORED
725	AAGGATCCTGCAGGCCAGGCAGTAGGCATCTCTTA!	EXON A
726	CCGAATTCTGCAGCAGAACATTGGCATTAGCAAAGC!	EXON A
771	CATCCGGGATGAAGAGTCAGGAGTCTGTGGCA!	EXONS B+A
772	ATACCCGGGCTGCAGACAAATGAGATTTCACACACCTGCG!	(SEQ ID NO: 116)
773	AAGGATCCTGCAGTTGGAACCTGCCACAGACTCCT!	(SEQ ID NO: 117)
776	ATACCCGGGCTGCAGATGAGATTACACACACCTGCGTGA!	(SEQ ID NO: 118)
		(SEQ ID NO: 119)

FIG. 23B  
PCR Primers for Factor I & Factor II

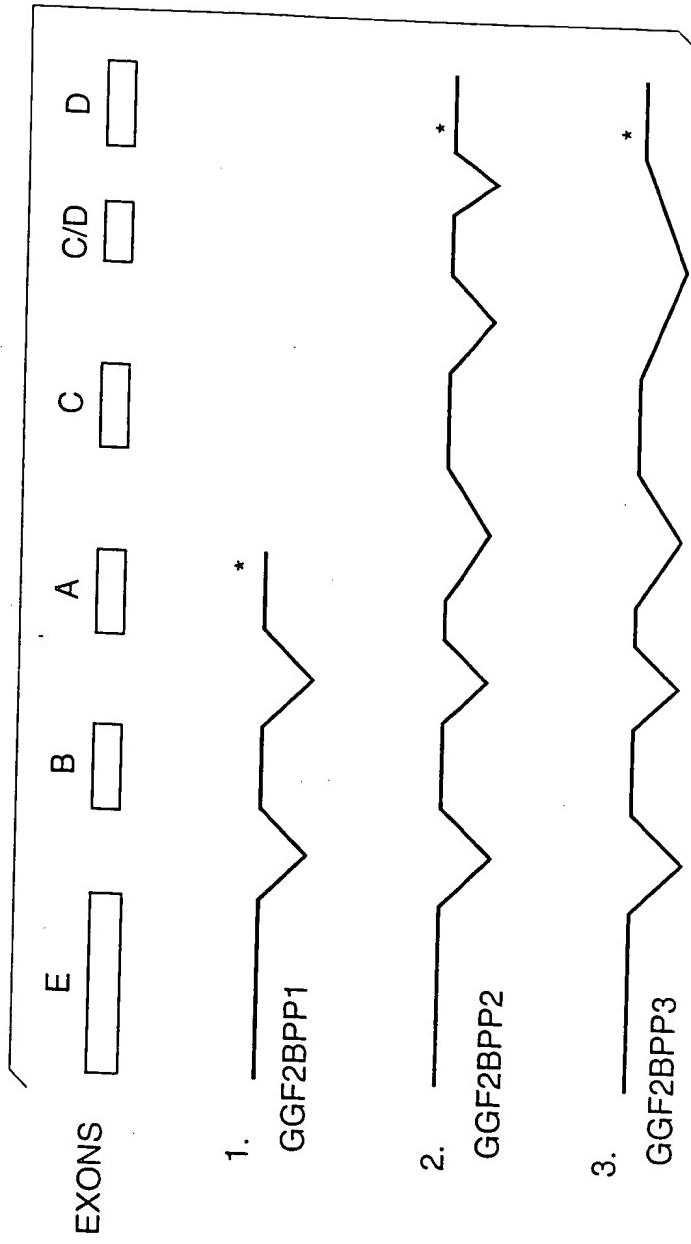
Unique PCR Primers for Factor II

**FIG. 24**  
**Summary of Contiguous GGF-II**  
**cDNA Structures & Sequences**



**FIG. 25**

**FIG. 26**  
**Alternative Gene Products of Putative Bovine GGF-II**



**FIG. 27****GGF-II Peptides Identified in Dduced Amino Acid Sequences of Putative Bovine GGF-II Proteins**

Peptide	Pos.	Sequence match	ID Sequences
II-1	1:	VHQVWAAK HQVWAAK AAGLK	(SEQ ID NO:120)
II-10	14:	_DLLLXV GGLKK dslltv RLGAW	(SEQ ID NO:121)
II-03	21:	LGAWGPPAFPVXY LLTVR lgawghpafpscglRKED	(SEQ ID NO:122) (SEQ ID NO:123)
II-02	41:	YIFFMEPEAXSSG KEDSR YIFFMEPEANSSG GPGRL	(SEQ ID NO:124) (SEQ ID NO:125)
II-6	103:	LVLR VAGSK LVLR CETSS	(SEQ ID NO:126)
I-18	112:	EYKCLKFKWFKKATVM CETSS eysslkfkwfkgnsel SRKNK	(SEQ ID NO:127) (SEQ ID NO:128)
II-12	151:	KASLADSGEYMXK ELRIS KASLADSGEYMCK VISKL	(SEQ ID NO:129) (SEQ ID NO:130)
I-07	152:	ASLADEYEYMRK LRISK asladsgeymck VISKL	(SEQ ID NO:131) (SEQ ID NO:132)

# FIG. 28A

SEQ ID NO: 133:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA	GCC GGG GGC TTG AAG AAG GAC TCG CTG	55
His Glu Val Trp Ala Ala Lys Ala Gly Leu Lys Asp Ser Leu		
CTC ACC GTG CGC CTG GGC GGC TGG GCG CAC CCC GCC TTC CCC TCC TGC	TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys		
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG		151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Met Glu Pro Glu		
GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC		199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro		
TCT CGA GAC GGC CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG		247
Ser Arg Asp Gly Pro Glu Pro Glu Pro Glu Gly Gly Gly Gly Pro Gly Ala Val		
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG		295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu		
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA		343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu		
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC		391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser		
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG		439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys		
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT		487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Lys Ala Asn Asp Ser Gly Glu Tyr		
ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC		535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn		
ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT		583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile		
TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT		625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr		
TGAATCACGC AGGTGTGTGA ATCTCATTC TGAAACAAATA AAAATCATGA AAGGAAAAAA		685
AATCGATGTC GACTCGAGAT GTGGCTGGAG GTCGACTCTA GAGGATCCC		744

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FIG. 28

## Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP2

SEQ ID NO: 134:

CCTGGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	GAC	TCG	CTG	55
His	Gln	Val	Trp	Ala	Ala	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Asp	Ser	Leu
CTC	ACC	GTG	CGC	CTG	GGC	GGC	TGG	GGC	CAC	CCC	GCC	TTG	CCC	TCC	TGC	103
Leu	Thr	Val	Arg	Leu	Gly	Ala	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG	151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glut	
GCC	AAC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Lys	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro	
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGG	GGT	CAG	CCG	GGT	GCT	GTG	247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val	
CAA	CGG	TGC	GGC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG	295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	
TAC	TCC	TCT	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	
CGA	AAG	AAC	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Gly	Gly	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Tyr	
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GCA	ATT	GAC	AGT	GCC	TCT	GCC	AAC	535
Met	Cys	Lys	Vai	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	

**FIG. 28C**

**Nucleotide Sequences & Deduced Amino Acid Sequences of GG2BPP2**

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr Ile Val Glu Ser Asn <u>Ala</u> Thr Ser Thr Ala Gly Thr	583
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	631
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	679
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	727
GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu	775
GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCACTC Val Ile Ala Ala Lys Thr Thr	826
CCTTTCTGTC TCTGCCGAA TAGGCCATCT CAGTCGGTGC CGCTTCTCTTG TTGCCGCATC TCCCCTCAGA TTCCCTCCTAG AGCTAGATGC GTTTTACCAAG GTCTAACATT GACTGCCCTCT	886
GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGGGTAAGG CTCCAGTGT TCTGAAATTG ATCTTGAAATT	946
ACTGTGATACT GACATGATAG TCCCTCTCAC CCAGTCAAT GACAATA <u>AAAG</u> GCCTTGAAA GTCAAAAAAA AAAAAAAA AAAAATCGA TGTGACTCG AGATGTGGCT GCAGGTCGAC	1066
TCTAGAG	1126
	1186
	1193

**FIG. 28D**

**Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPPP3**

SEQ ID NO: 135:

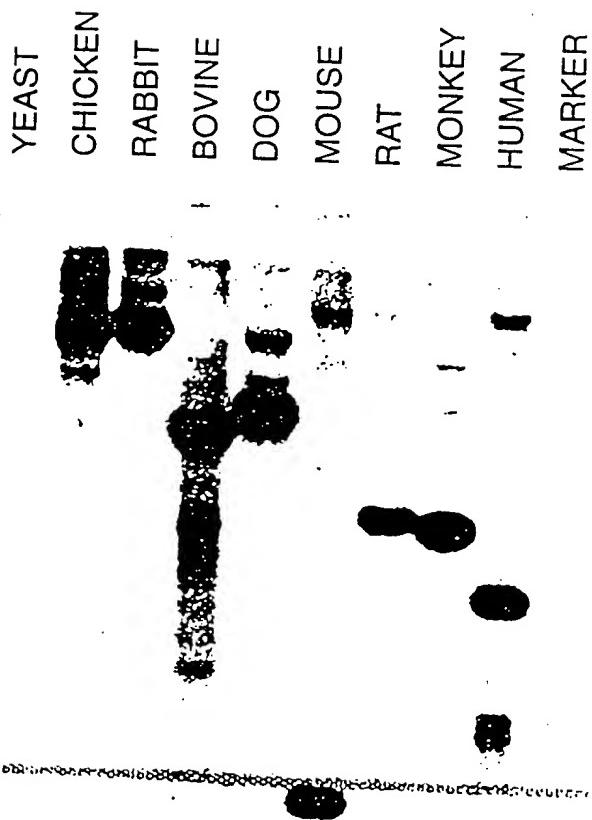
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG	GAC TCG CTG 55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Asp Ser Leu	
CTC ACC GTG CGC CTG GGC CCC TGG GGC CAC CCC GCC TTC CCC TCC TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC ATT GAG CCC GAG	151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
GCC AAC AGC AGC GGC GGG CCC CGC CGC CTT CCG AGC CTC CTT CCC CCC	199
Ala <u>Asn</u> <u>Ser</u> <u>Ser</u> Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CGG GGT GCT GTG	247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG	295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC	391
Tyr Ser Leu Lys Phe Lys Trp Phe Lys <u>Asn</u> <u>Gly</u> Ser Glu Leu Ser	
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG	439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Pro Lys	
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT	487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr	

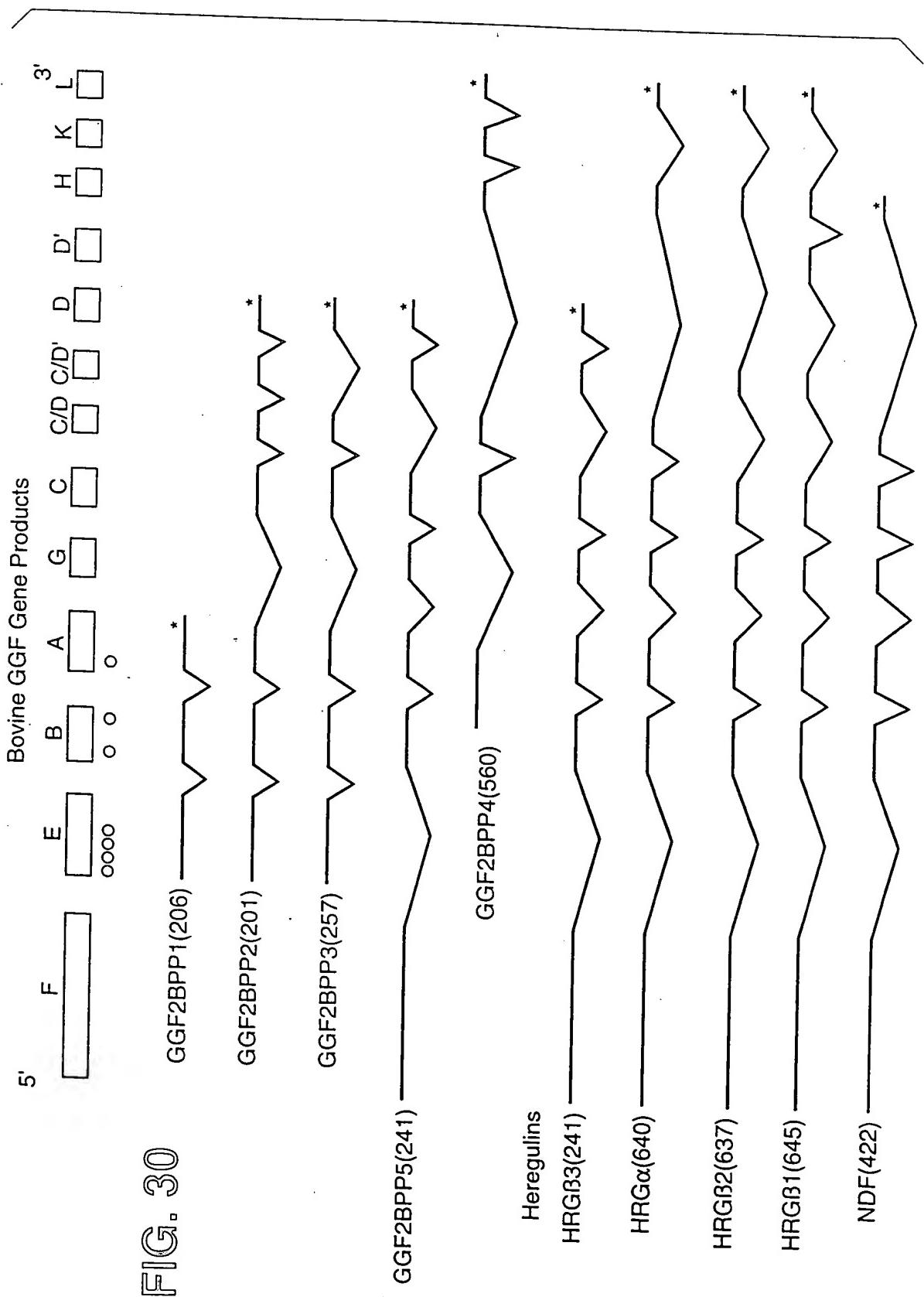
**FIG. 28E**

**Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPPP3**

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC	Met Cys Lys Val Ile Ser Lys Leu Gly Asn <u>Asp</u> Ser Ala Ser Ala Asn	535
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA	Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	583
AGC CAT CTT GTC AAG TGT GCA GAG AAG AAA ACT TTC TGT GTG ATT	Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	631
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	Gly Gly Glu Cys Pro Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	679
TTC TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	727
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CCT	Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro	775
GAA TAGGCCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAGA TTCCGCCCTAG	Glu	838
AGCTAGATGC GTTTTACAG GCTCTAACATT GACTGCCCT GCCTGTCGCA TGAGAACATT		
AACACAAGCG ATTGTATGAC TTCCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG		
GTGGCGTAAGG CTCCAGTGT TCTGAAATTG ATCTGAAATT ACTGTGATAAC GACATGATAG		
CCCCCTCTCAC CCAGTGCAAT GACA <u>ATAAAG</u> GCCTTGAAAAA GTCAAAAAAA AAAA		
AAAATCGAT GTCGACTCGA GATGTGGCTG		

**FIG. 29**





# FIG. 31A

**Coding Segments  
of Glial Growth  
Factor/Heregulin  
Gene**

CODING SEGMENT F: (SEQ ID NO: 136 (bovine) and 173 (human))

AGTTTCCCCC CCCAACTTGT CGGAACCTCTG GGCTCGCCG CAGGCAGGA GCGGAGGGC	60
GGCGGCTGCC CAGGGATGC GAGGGGGC CGGACGGTA TGGCCTCTCC CTCTCTGGGC	
TGGGAGGG CGGGACCGAG GCAGGGACAG GAGGGACCG CGGGGGAAC CGAGGAAC	120
CCAGGGCGC GCCAGGAGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCGCC	180
AGTCCAGGT GGCCGGGACC GCACGGTTGCG TCCCCGGCT CCCCCGGGCC GACAGGAGAC	240
GCTCCCCCCC ACGGCGGCC CGCCTCGGCC CGGTCGCTGG CCGCCTCCA CTCCGGGAC	300
CGCGAG CGCCTCAGCG CGCCCGCTCG CTCTC .CCC CTCGAGGGAC	
AAACTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGGCG TCGCCTTCGC	360
AAACTTTCC CAAACCCGAT CCGAGCCCTT GGACCAA.....C TCGCCTGC	
AAACTTTCC CGGAGCCGT CCGGCCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGA	420
CGAGAGCCGT CCGCGTAGAG CGCTC TCCGGCGAG ATG TCC GAG CGC AAA	
Glu Lys Lys Gly Lys Gly Lys Lys Asp Arg Gly Ser Gly	474
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG GAC AAG GAG CGA GGC TCC GGG	
GAA GGC AGA GGC AAA GGG AAG GGC AAG AAG GAG GAG CGA GGC TCC GGC	
R K E	
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala	522
AAG AAG CCC GTG CCC GCG GCT GGC GGC AGC CCA G	
AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA G	
S E	

30/78

## FIG. 31B

CODING SEGMENT E: (SEQ ID NO: 137)

CC	CAT	CAN	GTC	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	
His	Gln	Val	Trp	Ala	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	
CTG	CTC	ACC	GTC	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	
Leu	Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	
TGC	GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	
Cys	Gly	Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro
GAG	GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	
Glu	Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	
CCC	TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	
Pro	Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	
GTG	CAA	CGG	TGC	G												
Val	Gln	Arg	Cys													

FIG. 31C

CODING SEGMENT B: (SEQ ID NO: 138 (bovine, top) and 174 (human, bottom)

Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	Val	Ala	
CC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG	TCT	GTG	GCA
CC	TTG	CCT	CCC	CGA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	TGG	GCT	GCA

Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly
AAA	CCA	CAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GG
											K
AAA	CCA	CAA	AAT	ATC	AAG	ATA	CAA	AAA	AAG	CCA	GG

# FIG. 31D

CODING SEGMENT A: (SEQ ID NO: 139 (bovine) and 175 (human))

Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly  
G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA 46  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
G AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA  
N

Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser  
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT 94  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT

Ala Asn Ile Thr Ile Val Glu Ser Asn Ala  
GCC AAC ATC ACC ATT GTG GAG TCA AAC G 122  
||| ||| ||| ||| ||| ||| ||| |||  
GCC AAT ATC ACC ATC GTG GAA TCA AAC G

# FIG. 31E

CODING SEGMENT A' : (SEQ ID NO: 140)

TCTAAACTA CAGAGACTGT ATTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC  
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG 60  
Lys Ser Glu Leu Arg Ile Ser Lys Ala 110  
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA  
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu 158  
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT  
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly 206  
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC  
Lys Arg Cys Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile 254  
AAG GTA TGT GGT CAC ACT TGAATCACGCC AGGTGGTGA AATCTCATTG  
Lys Val Cys Gly His Thr 302  
TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTGA AATATCTTAT GGGTCCCT  
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATT 362  
417

# FIG. 31F

CODING SEGMENT G: (SEQ ID NO: 141 (bovine) and 176 (human))

Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser  
AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT 47  
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
AG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT  
I G

Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr  
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT 95  
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT ACT  
A

Ser Ser Ser  
TCT TCA T 102  
||| | | | |  
TCT TCA T

# FIG. 31G

CODING SEGMENT C: (SEQ ID NO: 160 (bovine) and 177 (human))

Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala  
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA 47  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
CT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG  
T

Glu Lys Glu Lys Thr Phe Cys Val Asn GLY GLU Cys Phe Met Val  
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG 95  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC TTC ATG GTG

Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys  
AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC 128  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC

# FIG. 31H

CODING SEGMENT C/D: (SEQ ID NO: 142 (bovine) and 178 (human))

Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro  
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC 48  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
AAG TGC CAA CCT GGA TTC ACT GGA GCA AGA TGT ACT GAG AAT GTG CCC

Met Lys Val Gln Thr Gln Glu  
ATG AAA GTC CAA ACC CAA GAA 69  
||| ||| ||| ||| ||| ||| |||  
ATG AAA GTC CAA AAC CAA GAA N

69

### **FIG. 31I**

CODING SEGMENT C/D' (SEQ ID NO: 143 (bovine) and 179 (human))

LYS	CYS	PRO	ASN	GLU	PHE	THR	GLY	ASP	ARG	CYS	Gln	ASN	Tyr	Val	Met
AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG
AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG

Ala	Ser	Phe	Tyr
GCC	AGC	TTC	TAC
GCC	AGC	TTC	TAC

60

(bovine and human)

CODING SEGMENT D: (SEQ ID NO: 144 (bovine) and 180 (human))

Ser	Thr	Ser	Pro	Phe	Leu	Ser	Leu	Pro	Glu	*
AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CCT	GAA	TAG
AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CCT	GAA	TAG

36

(human)

CODING SEGMENT D': (SEQ ID NO: 145 (bovine))

LYS	HIS	Leu	Gly	Ile	Glu	Phe	Met	Glu
AAG	CAT	CTT	GGG	ATT	GAA	TTT	ATG	GAG

27

# FIG. 31L

CODING SEGMENT H: (SEQ ID NO: 146 (bovine) and 484 (human))

Lys	Ala	Glu	Glu	Leu	Tyr	Gln	Lys	Arg	Val	Ile	Thr	Gly	Ile		
AAA	GGG	GAG	GAG	TTC	TAC	CAG	AAG	AGA	GTG	CTC	ACC	ATT	GGC	ATT	
														48	
AAG	GCG	GAG	GAG	CTG	TAC	CAG	AAG	AGA	GTG	CTG	ACC	ATA	ACC	GGC	ATC

Cys	Ile	Ala	Leu	Leu	Val	Val	Gly	Ile	Met	Cys	Val	Val	Tyr	Cys
TGC	ATC	GCG	CTG	CTG	GTT	GTC	GGC	ATC	ATG	TGT	GTG	GTC	TAC	TGC
														96
TGC	ATC	GCC	CTC	CTT	GTG	GTC	GGC	ATC	ATG	TGT	GTG	GCC	TAC	TGC

Lys	Thr	Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	Arg	Leu	Arg	Gln	Ser
AAA	ACC	AAG	AAA	CAA	CGG	AAA	AAG	CTT	CAT	GAC	CGG	CTT	CGG	CAG	AGC
AAA	ACC	AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	CGT	CTT	CGG	CAG	AGC

Leu	Arg	Ser	Glu	Arg	Asn	Thr	Met	Asn	Val	Ala	Asn	Gly	Pro	His	
CTT	CGG	TCT	GAA	AGA	AAC	ACC	ATG	ATG	AAC	GTA	GCC	AAC	GGG	CCC	CAC
CTT	CGG	TCT	GAA	CGA	AAC	ATG	ATG	ATG	AAC	ATT	GCC	AAT	GGG	CCT	CAC

His	Pro	Asn	Pro	Pro	Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	
CAC	CCC	AAT	CCG	CCC	CCC	GAG	AAC	GTG	CAG	CTG	GTG	AAT	CAA	TAC	GTA
CAT	CCT	AAC	CCA	CCC	CCC	GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	GTA

Ser	Lys	Asn	Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu
TCT	AAA	AAT	GTC	ATC	TCT	AGC	GAG	CAT	ATT	GTT	GAG	AGA	GAG	GCG	GAG
TCT	AAA	AAC	GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG

# FIG. 31M

Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr  
 AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT TCC ACT  
 ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 ACA TCC TTT TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT CAC TCC ACT  
 T

Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu  
 ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA  
 ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG AGC AAC GGA CAC ACT GAA  
 L

Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Val Glu  
 AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA  
 ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 AGC ATC CTT TCC GAA AGC CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA

Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn  
 AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC ATT  
 ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 AAC AGT AGG CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT ATT  
 T

Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg  
 GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA  
 ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA  
 T

Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg  
 GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT GAA AG  
 ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT AGT GAA AG

# FIG. 31N

CODING SEGMENT K: (SEQ ID NO: 161)

A	CAT	AAC	CTT	ATA	GCT	GAG	CTA	AGG	AGA	AAC	AAG	GCC	CAC	AGA	TCC
His	Asn	Leu	Ile	Ala	Glu	Leu	Arg	Arg	Asn	Lys	Ala	His	Arg	Ser	
AAA	TGC	ATG	CAG	ATC	CAG	CTT	TCC	GCA	ACT	CAT	CTT	AGA	GCT	TCT	TCC
Lys	Cys	Met	Gln	Ile	Gln	Leu	Ser	Ala	Thr	His	Leu	Arg	Ala	Ser	Ser
AT <sup>T</sup>	CCC	CAT	TGG	GCT	TCA	TTC	TCT	AAG	ACC	CCT	TGG	CCT	TTA	GGA	AG
Ile	Pro	His	Trp	Ala	Ser	Phe	Ser	Lys	Thr	Pro	Trp	Pro	Leu	Gly	Arg

# FIG. 310

CODING SEGMENT L: (SEQ ID NO: 147 (bovine) and 182 (human))

Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp	
G	TAT	GTA	TCA	GCA	ATG	ACC	ACC	GCT	GCT	CGT	ATG	TCA	CCT	GTA	GAT
															46
G	TAT	GTG	TCA	GCC	ATG	ACC	ACC	GCT	GCT	CGT	ATG	TCA	CCT	GTA	GAT
Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro
TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAG	TCA	CCC	CCT	TCG	GAA	ATG	TCC	CCG
															94
TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAA	TCG	CCC	CCT	TCG	GAA	ATG	TCT	CCA
Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro
CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	TCC	ATG	GCG	GTC	AGT	CCC
															142
CCC	GTG	TCC	AGC	ATG	ACG	GTG	TCC	ATG	CCT	ATG	GCG	GTC	AGC	CCC	N
Phe	Val	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	Arg	Leu
TTC	GTG	GAA	GAG	GAG	AGA	CCC	CTG	CTG	CTC	CTT	GTG	ACG	CCA	CGG	CTG
															190
TTC	ATG	GAA	GAG	GAG	CTT	CTA	CTT	CTC	GTG	ACA	CCA	CCA	AGG	CTG	N
Arg	Glu	Lys	-	Tyr	Asp	His	His	Ala	Gln	Gln	Phe	Asn	Ser	Phe	His
CGG	GAG	AAG	...	TAT	GAC	CAC	CAC	GCC	CAG	CAA	TTC	AAC	TCG	TTC	CAC
CGG	GAG	AAG	AAG	TTT	GAC	CAT	CAC	CCT	CAG	CAG	TTC	AGC	TCC	TTC	CAC
Cys	Asn	Pro	Ala	His	Glu	Ser	Asn	Ser	Leu	Pro	Pro	Ser	Pro	Leu	Arg
TGC	AAC	CCC	GCG	CAT	GAG	AGC	AAC	AGC	CTG	CCC	CCC	AGC	CCC	TTG	AGG
CAC	AAC	CCC	GCG	CAT	GAC	AGT	AAC	AGC	CTC	CCT	GCT	AGC	CCC	TTG	AGG
					D										A
															N

# FIG. 31P

Ile	Val	Glu	Asp	Glu	Glu	Tyr	Glu	Thr	Gln	Glu	Tyr	Glu	Pro	Ala	
ATA	GTG	GAG	GAT	GAG	GAA	TAT	GAA	ACG	ACC	CAG	GAG	TAC	GAA	CCA	GCT
															334
ATA	GTG	GAG	GAT	GAG	GAG	TAT	GAA	ACG	ACC	CAA	GAG	TAC	GAG	CCA	GCC
Gln	Glu	Pro	Val	Lys	Lys	Leu	Thr	Asn	Ser	Arg	Arg	Ala	Lys	Arg	
CAA	GAG	CCG	GTT	AAG	AAA	CTC	ACC	AAC	AGC	AGC	CGG	CGG	GCC	AAA	AGA
															382
CAA	GAG	CCT	GTT	AAG	AAA	CTC	GCC	AA.	...T	AGC	CGG	CGG	GCC	AAA	AGA
							A			V				S	
Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	His	Arg	Leu	Glu	Met	Asp	Asn	Asn
ACC	AAG	CCC	AAT	GGT	CAC	ATT	GCC	CAC	AGG	TTG	GAA	ATG	GAC	AAC	AAC
															430
ACC	AAG	CCC	AAT	GGC	CAC	ATT	GCT	AAC	AGA	TTG	GAA	GTG	GAC	AGC	AAC
Thr	Gly	Ala	Asp	Ser	Ser	Asn	Ser	Glu	Ser	Glu	Thr	Glu	Asp	Glu	Arg
ACA	GGC	GCT	GAC	AGC	AGT	AAC	TCA	GAG	AGC	GAA	ACA	GAG	GAT	GAA	AGA
ACA	AGC	TCC	CAG	AGC	AGT	AAC	TCA	GAG	AGT	GAA	ACA	GAA	GAT	GAA	AGA
S	S	Q													

**FIG. 31Q**

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## FIG. 31R

ATG	AGA	TGG	CGA	GCC	CCG	CGC	TCC	GGG	CGT	CCC	GGC	CCC	CGG	48	
Met	Arg	Trp	Arg	Arg	Ala	Pro	Arg	Arg	Ser	Gly	Arg	Pro	Gly	Pro	Arg
GCC	CAG	CGC	CCC	GGC	TCC	GCC	CGC	TCG	CCG	CTG	CCG	CTG	CCG	CTG	96
Ala	Gln	Arg	Pro	Gly	Ser	Ala	Ala	Arg	Ser	Pro	Pro	Leu	Pro	Leu	Leu
HUMAN CODING SEGMENT E: CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG CTC GCG CCG GGG GCG 144 (SEQ ID NO: 163)															
GGC	GCC	GGC	AAC	GAG	GCG	GCT	CCC	GGG	GCC	TCG	GCG	CCG	GCG	192	
Ala	Ala	Gly	Asn	Glu	Ala	Ala	Pro	Ala	Gly	Ala	Ser	Val	Cys	Tyr	Ser
TCC	CCG	CCC	AGC	GTG	GGG	TCG	CAG	GAG	CTA	GCT	CAG	CGC	GCC	GCG	240
Ser	Pro	Pro	Ser	Val	Gly	Ser	Val	Gly	Glu	Leu	Ala	Gln	Arg	Ala	Ala
GTG	GTG	ATC	GAG	GGG	AAG	GTG	CAC	CCG	CAG	CCG	CAG	CAG	GGG	GCA	288
Val	Val	Val	Glu	Gly	Lys	Val	His	Pro	Gln	Arg	Arg	Gln	Gly	Ala	
CTC	GAC	AGG	AAG	GCG	GCG	GCG	GCG	GCG	GAG	GCA	GGG	GGC	TGG	GCC	336
Leu	Asp	Asp	Arg	Lys	Ala	Ala	Ala	Ala	Gly	Glu	Ala	Gly	Ala	Trp	Gly
GGC	GAT	CGC	GAG	CCG	CCA	GCC	GCG	GCG	CCA	CGG	GCG	CTG	GGG	CCC	384
Gly	Asp	Arg	Glu	Pro	Pro	Ala	Ala	Gly	Pro	Arg	Ala	Leu	Gly	Pro	Pro
GCC	GAG	GAG	CCG	CTG	CTC	GCC	GCC	AAC	GGG	ACC	GTG	CCC	TCT	TGG	432
Ala	Glu	Glu	Pro	Leu	Leu	Ala	Ala	Asn	Gly	Thr	Val	Pro	Ser	Trp	Pro
ACC	GCC	CCG	GTG	CCC	AGC	GCC	GGC	GAG	CCC	GGG	GAG	GCC	CCC	TAT	480
Thr	Ala	Pro	Vai	Pro	Ser	Ala	Gly	Glu	Pro	Gly	Glu	Glu	Ala	Pro	Tyr
CTG	GTG	AAG	GTG	CAC	CAG	GTG	TGG	GCG	GTG	AAA	GCC	GGG	GGC	TTG	528
Leu	Val	Lys	Val	His	Gln	Val	Trp	Ala	Val	Lys	Ala	Gly	Gly	Leu	Lys
AAG	GAC	TGC	CTG	CTC	ACC	GTG	CGC	CTG	GGG	ACC	TGG	GGC	CAC	CCC	576
LYS	Asp	Ser	Leu	Leu	Thr	Val	Arg	Leu	Gly	Thr	Trp	Gly	His	Pro	Ala
TTC	CCC	TCC	TGC	GGG	AGG	CTC	AAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	624
Phe	Pro	Ser	Cys	Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Thr	Phe	Phe
ATG	GAG	CCC	GAC	AAC	AGC	ACC	AGC	CGC	CGG	CGG	CGG	TTC	CGA	672	
Met	Glu	Pro	Asp	Ala	Asn	Ser	Thr	Ser	Arg	Ala	Pro	Ala	Ala	Phe	Arg
GCC	TCT	TTC	CCC	CCT	CTG	GAG	ACG	GCG	CGG	AAC	CTC	AAG	GAG	GTC	720
Ala	Ser	Phe	Pro	Pro	Leu	Glu	Thr	Gly	Arg	Asn	Leu	Lys	Lys	Glu	Val
AGC	CGG	GTG	CTG	TGC	AAG	CGG	TGC	G							745
Ser	Arg	Val	Leu	Cys	Lys	Arg	Cys								

**FIG. 32A**

**GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence**

SEQ ID NO: 148:

AGTTTCCCCC	CCCAACTTGT	CGGAACCTG	GGCTCCGGCG	CAGGGAGGA	GCGGAGGGC	60	
GGGGCTGCC	CAGGGATGTC	GAGGGGGGC	CGGACGGTAA	TGGCCTCTCC	CTCCTCGGGC	120	
TGGAGGGCG	CCGGACCGAG	GCAGCGACAG	GAGGGACCG	GGGGGAAAC	CGAGGACTCC	180	
CCAGGGGGC	GCCAGCAGGA	GCCACCCCGC	GAGCGTGGGA	CGGGGACGG	GCGCCCGCCA	240	
GTCCCAGGTG	GCCCCGACCG	CACGTTGGGT	CCCCGGCTC	CCCCGGCG	ACAGGAGACG	300	
CTCCCCCCA	CGCCGGCGC	GCCTGGCCC	GGTCGGTGGC	CGGCCTCCAC	TCCGGGACA	360	
AACTTTCCC	GAAGCCGATC	CCAGGCCCTCG	GACCCAAACT	TGTGGCGGT	CGGCCTCGCC	420	
GGGAGCCGTC	CGGCCAGAGC	GTGCACTTCT	CGGGGAG	ATG TCG	GAG CGC AGA	475	
			Met Ser Glu Arg Arg				
GAA	GGC AAA	GGC AAG	GGG AAG	GAC AAG	GAC CGA	GGC TCC GGG	523
Glu	Gly Lys	Gly Lys	Gly Lys	Gly Lys	Arg Gly	Ser Gly	
AAG	CCC GTG	CCC GCG	GCT GGC	CGC AGC	CCA GCC	TTG CCTT CCC	571
LYS	Pro Val	Pro Ala	Ala Gly	Gly Pro	Ser Pro	Ala Leu	
CGC	TTC	AAA GAG	ATG AAG	CAG ATG	TCT GCA	Pro Pro	
Arg	Leu	Lys Glu	Met Glu	Ser Ser	Val Ala	AAA GGT TCC	619
GTG	CTT CGG	TGC GAG	ACC AGT	TCT GAA	TAC TCC	CTC AAG TTC	
Val	Leu	Arg Cys	Glu Thr	Ser Ser	Glu Tyr	Ser Leu	
TGG	TTC AAG	AAT GGG	AGT GAA	RTA AGC	CGA AAG	AAA CCA CAA	
Trp	Phe Lys	Asn Gly	Ser Glu	Leu Ser	Arg Lys	Pro Asn Lys	
ATC	AAG ATA	CAG AAA	AGG CCG	GAG TCA	GAA CTT CGC	ATT AGC AAA	
Ile	Lys Ile	Gln Lys	Arg Pro	Gly Lys	Ser Glu	Leu Arg Ile	
GGC	TCA CTG	GCT GAT	TCT GGA	GAA TAT	ATG TGC	AAA GTG ATC	
Ala	Ser Leu	Ala Asp	Ser Ser	Gly Glu	Tyr Met	Cys Lys Val	
						Ser Ser Lys	

**FIG. 32B**  
GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

**FIG. 33A**

**GGF2BPPP2 Nucleotide Sequence & Deduced Protein Sequence**

SEQ ID NO: 149:

CAT CAN GTG TGG GCG AAA GCC	GGG GGC TTG AAG AAG GAC	TCG CTG	48
His Gln Val Trp Ala Ala Lys	Gly Gly Leu Lys Asp Ser Leu		
CTC ACC GTG CGC CTG GGC GCC	TGG GGC CAC CCC GCC TTC CCC	TCC TCC	96
Leu Thr Val Arg Leu Gly Ala	Trp Gly His Pro Ala Phe Pro	Ser Cys	
GGG CGC CTC AAG GAG GAC AGC	AGG TAC ATC TTC TTG GAG CCC	GAG CCC	144
Gly Arg Leu Lys Glu Asp Ser	Arg Tyr Ile Phe Met Glu Pro	Glu Pro	
GCC AAC AGC AGC GGC GGG CCC	GGC CGC CTT CCG AGC CTC CTT CCC CCC	CCC CCC	192
Ala Asn Ser Ser Gly Pro Gly	Pro Gly Arg Leu Pro Ser Leu	Leu Pro	
TCT CGA GAC GGG CCG GAA CCT	CAA GAA GGA GGT CAG CCG GGT GCT GTG	GCT GTG	240
Ser Arg Asp Gly Pro Glu Pro	Gln Pro Glu Gly Gln Pro Gly Ala Val		
CAA CGG TGC GCC TTG CCT CCC	CGC TTG AAA GAG ATG AAG AGT CAG GAG	CAG GAG	288
Gln Arg Cys Ala Leu Pro Pro	Arg Leu Lys Glu Met Lys Ser Gln Glu		
TCT GTG GCA GGT TCC AAA CTA	GTG CTT CGG TGC GAG ACC AGT TCT GAA	TCT GAA	336
Ser Val Ala Gly Ser Lys Leu	Val Leu Arg Cys Glu Thr Ser Ser	Glu Leu Ser	
TAC TCC TCT CTC AAG TTC AAG	TGG TTC AAG AAT GGG AGT GAA TTA AGC	AGC	384
Tyr Ser Ser Leu Lys Phe Lys	Trp Phe Lys Asn Gly Ser Glu		
CGA AAG AAC AAA CCA GAA AAC	ATC AAG ATA CAG AAA AGG CCG GGG AAG	AAG	432
Arg Lys Asn Lys Pro Glu Asn	Ile Lys Ile Gln Lys Arg Pro Gly Lys		
TCA GAA CTT CGC ATT AGC AAA	GCG TCA CTG GCT GAT TCT GGA GAA TAT	TAT	480
Ser Glu Leu Arg Ile Ser Lys	Ala Ser Leu Ala Asp Ser Gly Glu Tyr		
ATG TGC AAA GTG ATC AGC AAA	CTA GGA AAT GAC AGT GCC TCT GCC AAC	AAC	528
Met Cys Lys Val Ile Ser Lys	Leu Gly Asn Asp Ser Ala Ser Ala Asn		

**FIG. 33B**  
GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence

**FIG. 34A**

**GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence**

SEQ ID NO: 150:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GAT TCT GGA GAA	49
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	
TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC	97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	
AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG	145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	
ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG AAA ACT TTC TGT GTG	193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	
AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA	241
Asn Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	
TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG	289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC	337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr	
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTC TAC	385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	
GTT GGC ATC ATG TGT GTG GTG TAC TAC TGC AAA ACC AAG AAA CAA CGG	433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg	
AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC	481
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn	
ACC ATG ATG AAC AAC GCC AAC GGG CCC CAC CCC AAT CCG CCC CCC	529
Thr Met Met Asn Val Ala Asn Gly Pro His Pro Asn Pro Pro Pro	
GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT	577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser	

**FIG. 34B**

**GGF2BPPP4 Nucleotide Sequence & Deduced Protein Sequence**

AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT	Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser	625
CAC TAC ACT TCG ACA GCT CAT TCC ACT GTC ACT CAG ACT CCC	Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro	673
AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC	Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Ser Glu Ser	721
CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC	His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser	769
CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT	Pro Thr Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg	817
GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC	Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr	865
CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG	Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg	913
AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA	Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala	961
ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG	Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys	1009
ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT	Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala	1057
CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC	Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro	1105
CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG GTC TCC ATG CCC	Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro	1153

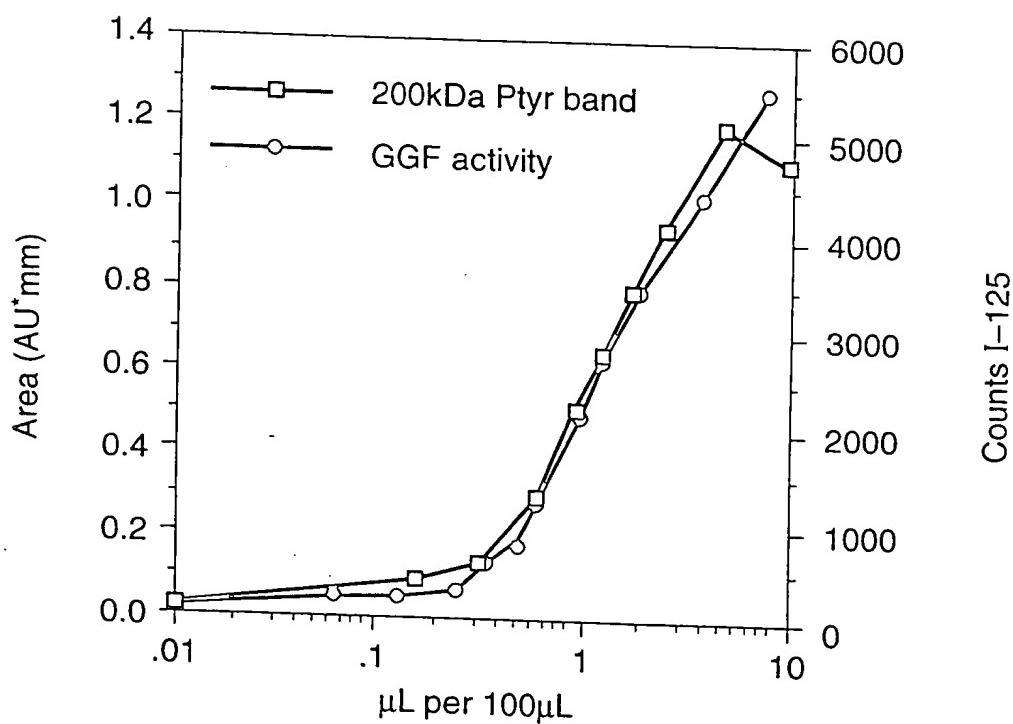
FIG. 34C

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

# FIG. 35

GGF2bpp5 (SEQ ID NO: 151) KCAEKEKTFCVNGGECECFMVKDLLSNPSRYLCKCPNEFTGDRCQNYVMASFY  
GGF2bpp4 (SEQ ID NO: 152) KCAEKEKTFCVNGGDCFMVKDLLSNPSRYLCKCQPGFTGARCTENVPMKVQ  
hEGF (SEQ ID NO: 153) ECLRKYKDFCIH-GECKYVVKELRAPS---CKCQQEYFGERCGEKSNKTHS

**FIG. 36**  
200 kDa Tyrosine Phosphorylation  
Compared with Mitogenic Activity



**FIG. 37A GGF/Heregulin Splicing Variants**

F-B-A'

F-B-A-C-C/D-D  
 F-B-A-C-C/D-H  
 F-B-A-C-C/D-H-L  
 F-B-A-C-C/D-H-K-L  
 F-B-A-C-C/D-D'-H  
 F-B-A-C-C/D-D'-H-L  
 F-B-A-C-C/D-D'-H-K-L  
 F-B-A-C-C/D'-D  
 F-B-A-C-C/D'-H  
 F-B-A-C-C/D'-H-L  
 F-B-A-C-C/D'-H-K-L  
 F-B-A-C-C/D'-D'-H  
 F-B-A-C-C/D'-D'-H-L  
 F-B-A-C-C/D'-D'-H-K-L  
 F-B-A-C-C/D-C/D'-D  
 F-B-A-C-C/D-C/D'-H  
 F-B-A-C-C/D-C/D'-H-L  
 F-B-A-C-C/D-C/D'-H-K-L  
 F-B-A-C-C/D-C/D'-H-L  
 F-B-A-C-C/D-C/D'-D'-H  
 F-B-A-C-C/D-C/D'-D'-H-L  
 F-B-A-C-C/D-C/D'-D'-H-K-L  
 F-B-A-C-C/D-C/D'-D'-H-L  
 F-B-A-C-C/D-C/D'-D'-H-K-L

F-B-A-G-C-C/D-D  
 F-B-A-G-C-C/D-H  
 F-B-A-G-C-C/D-H-L  
 F-B-A-G-C-C/D-H-K-L  
 F-B-A-G-C-C/D-D'-H  
 F-B-A-G-C-C/D-D'-H-L  
 F-B-A-G-C-C/D-D'-H-K-L  
 F-B-A-G-C-C/D'-D  
 F-B-A-G-C-C/D'-H  
 F-B-A-G-C-C/D'-H-L  
 F-B-A-G-C-C/D'-H-K-L  
 F-B-A-G-C-C/D'-D'-H  
 F-B-A-G-C-C/D'-D'-H-L  
 F-B-A-G-C-C/D'-D'-H-K-L  
 F-B-A-G-C-C/D-C/D'-D  
 F-B-A-G-C-C/D-C/D'-H  
 F-B-A-G-C-C/D-C/D'-H-L  
 F-B-A-G-C-C/D-C/D'-H-K-L  
 F-B-A-G-C-C/D-C/D'-D'-H  
 F-B-A-G-C-C/D-C/D'-D'-H-L  
 F-B-A-G-C-C/D-C/D'-D'-H-K-L  
 F-B-A-G-C-C/D-C/D'-D'-H  
 F-B-A-G-C-C/D-C/D'-D'-H-L  
 F-B-A-G-C-C/D-C/D'-D'-H-K-L

F-E-B-A'

F-E-B-A-C-C/D-D  
 F-E-B-A-C-C/D-H  
 F-E-B-A-C-C/D-H-L  
 F-E-B-A-C-C/D-H-K-L  
 F-E-B-A-C-C/D-D'-H  
 F-E-B-A-C-C/D-D'-H-L  
 F-E-B-A-C-C/D-D'-H-K-L  
 F-E-B-A-C-C/D'-D  
 F-E-B-A-C-C/D'-H  
 F-E-B-A-C-C/D'-H-L  
 F-E-B-A-C-C/D'-H-K-L  
 F-E-B-A-C-C/D'-D'-H  
 F-E-B-A-C-C/D'-D'-H-L  
 F-E-B-A-C-C/D'-D'-H-K-L  
 F-E-B-A-C-C/D-C/D'-D  
 F-E-B-A-C-C/D-C/D'-H  
 F-E-B-A-C-C/D-C/D'-H-L  
 F-E-B-A-C-C/D-C/D'-H-K-L  
 F-E-B-A-C-C/D-C/D'-D  
 F-E-B-A-C-C/D-C/D'-H  
 F-E-B-A-C-C/D-C/D'-H-L  
 F-E-B-A-C-C/D-C/D'-D'-H  
 F-E-B-A-C-C/D-C/D'-D'-H-L  
 F-E-B-A-C-C/D-C/D'-D'-H-K-L

F-E-B-A-G-C-C/D-D  
 F-E-B-A-G-C-C/D-H  
 F-E-B-A-G-C-C/D-H-L  
 F-E-B-A-G-C-C/D-H-K-L  
 F-E-B-A-G-C-C/D-D'-H  
 F-E-B-A-G-C-C/D-D'-H-L  
 F-E-B-A-G-C-C/D-D'-H-K-L  
 F-E-B-A-G-C-C/D'-D  
 F-E-B-A-G-C-C/D'-H  
 F-E-B-A-G-C-C/D'-H-L  
 F-E-B-A-G-C-C/D'-H-K-L  
 F-E-B-A-G-C-C/D'-D'-H  
 F-E-B-A-G-C-C/D'-D'-H-L  
 F-E-B-A-G-C-C/D'-D'-H-K-L  
 F-E-B-A-G-C-C/D-C/D'-D  
 F-E-B-A-G-C-C/D-C/D'-H  
 F-E-B-A-G-C-C/D-C/D'-H-L  
 F-E-B-A-G-C-C/D-C/D'-H-K-L  
 F-E-B-A-G-C-C/D-C/D'-D'-H  
 F-E-B-A-G-C-C/D-C/D'-D'-H-L  
 F-E-B-A-G-C-C/D-C/D'-D'-H-K-L

**FIG. 37B**  
**GGF/Heregulin**  
**Splicing Variants**

E-B-A'

E-B-A-C-C/D-D  
 E-B-A-C-C/D-H  
 E-B-A-C-C/D-H-L  
 E-B-A-C-C/D-H-K-L  
 E-B-A-C-C/D-D'-H  
 E-B-A-C-C/D-D'-H-L  
 E-B-A-C-C/D-D'-H-K-L  
 E-B-A-C-C/D'-D  
 E-B-A-C-C/D'-H  
 E-B-A-C-C/D'-H-L  
 E-B-A-C-C/D'-H-K-L  
 E-B-A-C-C/D'-D'-H  
 E-B-A-C-C/D'-D'-H-L  
 E-B-A-C-C/D'-D'-H-K-L  
 E-B-A-C-C/D-C/D'-D  
 E-B-A-C-C/D-C/D'-H  
 E-B-A-C-C/D-C/D'-H-L  
 E-B-A-C-C/D-C/D'-H-K-L  
 E-B-A-C-C/D-C/D'-H  
 E-B-A-C-C/D-C/D'-D'-H  
 E-B-A-C-C/D-C/D'-D'-H-L  
 E-B-A-C-C/D-C/D'-D'-H-K-L

E-B-A-G-C-C/D-D  
 E-B-A-G-C-C/D-H  
 E-B-A-G-C-C/D-H-L  
 E-B-A-G-C-C/D-H-K-L  
 E-B-A-G-C-C/D-D'-H  
 E-B-A-G-C-C/D-D'-H-L  
 E-B-A-G-C-C/D-D'-H-K-L  
 E-B-A-G-C-C/D'-D  
 E-B-A-G-C-C/D'-H  
 E-B-A-G-C-C/D'-H-L  
 E-B-A-G-C-C/D'-H-K-L  
 E-B-A-G-C-C/D'-D'-H  
 E-B-A-G-C-C/D'-D'-H-L  
 E-B-A-G-C-C/D'-D'-H-K-L  
 E-B-A-G-C-C/D-C/D'-D  
 E-B-A-G-C-C/D-C/D'-H  
 E-B-A-G-C-C/D-C/D'-H-L  
 E-B-A-G-C-C/D-C/D'-H-K-L  
 E-B-A-G-C-C/D-C/D'-D'-H  
 E-B-A-G-C-C/D-C/D'-D'-H-L  
 E-B-A-G-C-C/D-C/D'-D'-H-K-L  
 E-B-A-G-C-C/D-C/D'-D'-H-L

# FIG. 38

## EGFL1

SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTC TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT	192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro	
GAA TAG	
Glut	

# FIG. 39

## EGFL2

SEQ ID NO: 155:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTC	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
GGA	GGC	GAG	TGC	TTC	ATG	GTC	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
TTG	TGC	AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	144
Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	
GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAA	GCG	GAG	GAG	CTC	TAC	TAA	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Ala	Glu	Glu	Leu	Tyr		

# FIG. 40

## EGFL3

SEQ ID NO: 156:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn
															48
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr
															96
TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr
															144
GTA	ATG	GCC	AGC	TTC	TAC	AAA	GCG	GAG	CTC	TAC	TAA				
Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	Glu	Leu	Tyr				183

**FIG. 41**  
**EGFL4**

SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG AAA ACT TTC TGT GTG AAT  
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 48  
  
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC  
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr 96  
  
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC  
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr 144  
  
GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA  
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys 192  
  
GCG GAG GAG CTC TAC TAA  
Ala Glu Glu Leu Tyr 210

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FIG. 42  
EGFL5

SEQ ID NO: 158:

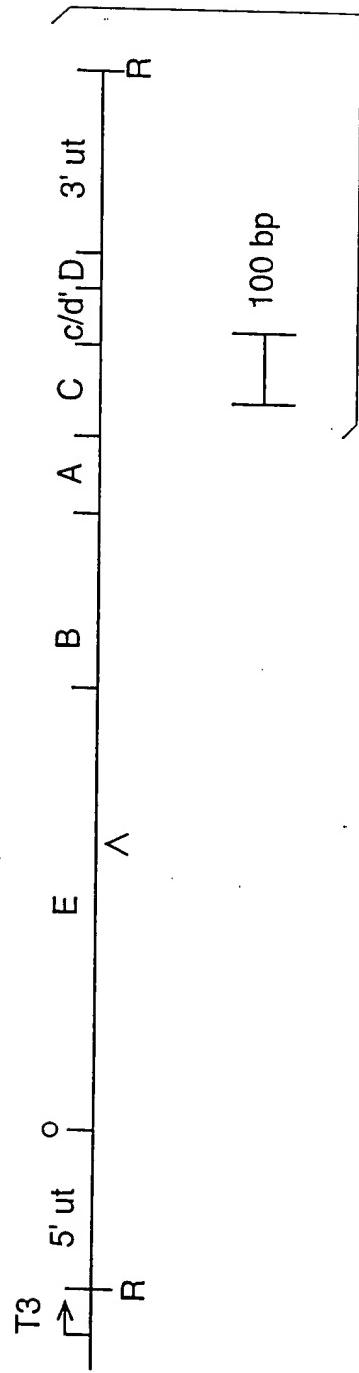
AGC CAT CTT GTC AAG TGT GCA GAG AAG AAA ACT	96	TTC	TGT	GTG	AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn						
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC						
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr						
TTC TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT						
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn						
GTC CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT						
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr						
GTT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TAC TAC AGT ACG TCC						
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser						
ACT CCC TTT CTG TCT CCT GAA TAG						
Thr Pro Phe Leu Ser Leu Pro Glu						

**FIG. 43**  
**EGFL6**

SEQ ID NO: 159:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
CGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTC TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Ileu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
CTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT	192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr	
GCT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG	240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu	
GAG CTC TAC TAA	252
Glu Leu Tyr	

**FIG. 44**  
GGF2HBS5



**FIG. 45A**  
**Nucleotide Sequence & Deduced Acid Sequence of GGF2HBSS5**

SEQ ID NO: 21:								
GGAAATTCCCTT TTTTTTTTTT TTTCCTTCTT NNTTTTTTTT TGCCCTTATA CCTCTTCGCC	60							
TTTCTGTGGT TCCATCCACT CCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT								
GCACCCCCAA TAAATAATAA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGGTGCTG	120							
CGAGGGAAAG GAAAAGGGAG GCAGGGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC	180							
AGAAGCCCCG ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC	240							
Met Arg Trp Arg Ala Pro Arg Arg Arg	291							
TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC								
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg	339							
TCG TCG CCG CTG CCG CTG CTG CCA CTA CTG CTG CTG CTG CTG GGG ACC								
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Gly Thr	387							
Val Cys Leu Leu Thr Val GGF-II 09								
GCG GCC CTG GCG CCG GGG GCG GCG GCC GGC AAC GAG GCG GCT CCC GCG								
Ala Ala Leu Ala Pro Gly Ala Ala Gly Asn Glu Ala Ala Pro Ala	435							
Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Val Ser Val Gly Ser Val Gln	GGF-II 08							
GAG CTA GCT CAG CGC  GCC GCG GTG ATC GAG GGA AAG GTG CAC CCG								
Glu Leu Ala Gln Arg Ala Ala Val Val Ile Glu Gly Lys Val His Pro	531							
Glu Leu Val Gln Arg Trp Phe Val Val Ile Glu Gly Lys Val Lys	GGF-II 04							

## FIG. 45B

### Nucleotide Sequence & Deduced Acid Sequence of GGF2HBSS5

CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG	579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala	
GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GCG	627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly	
CCA CGG CGG CTG GGG CCG CCC GCC GAG CCG CTG CTC GCC GCC AAC	675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn	
GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG	723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu	
CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG	771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala	
Lys Val His Glu Val Trp Ala GGF-II 01 & GGF-II 11	
GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG	819
Val Lys Ala Gly Gly Leu Lys Asp Ser Leu Leu Thr Val Arg Leu	
Ala Lys Asp Leu Leu Xaa Val Leu GGF-II 10	
GGG ACC TGG GGC CAC CCC GCC TTC TCC TGC GGG AGG CTC AAG GAG	867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu	
Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr GGF-II 03	
GAC AGC AGG TAC ATC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC	915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser	
Tyr Ile Phe Phe Met Glu Pro Gla Ala Xaa Ser Ser Gly GGF-II 02	

# FIG. 45C

## Nucleotide Sequence & Deduced Acid Sequence of GGF2HBSS

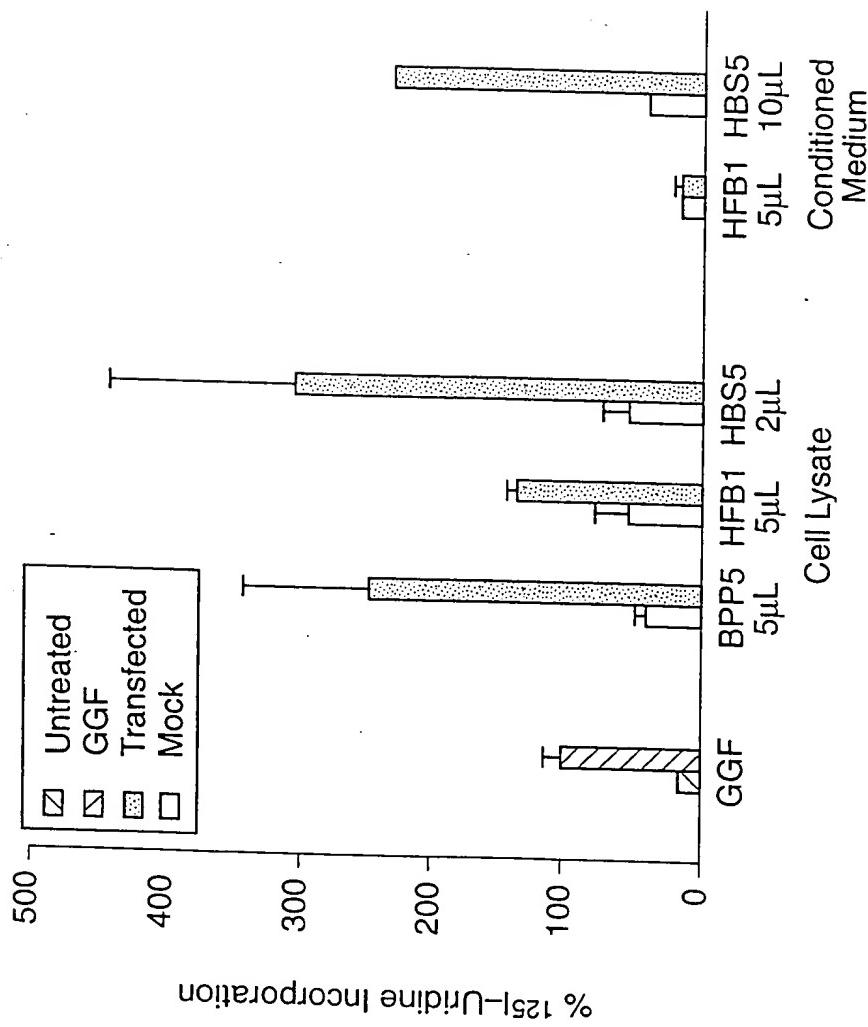
CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC	963
Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly	
CGG AAC CTC AAG AAG GAG GTC AGC CGG CGG GTG CTG TGC AAG CGG TGC GCC	1011
Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala	
TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT	1059
Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly	
TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC	1107
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu	
Leu Val Leu Arg GGF-II 06	
AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA	1155
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys	
CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC	1203
Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg	
ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG	1251
Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val	
Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys GGF-II 12	
ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG	1299
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val	
GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA	1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Gly Thr Ser His Leu Val	

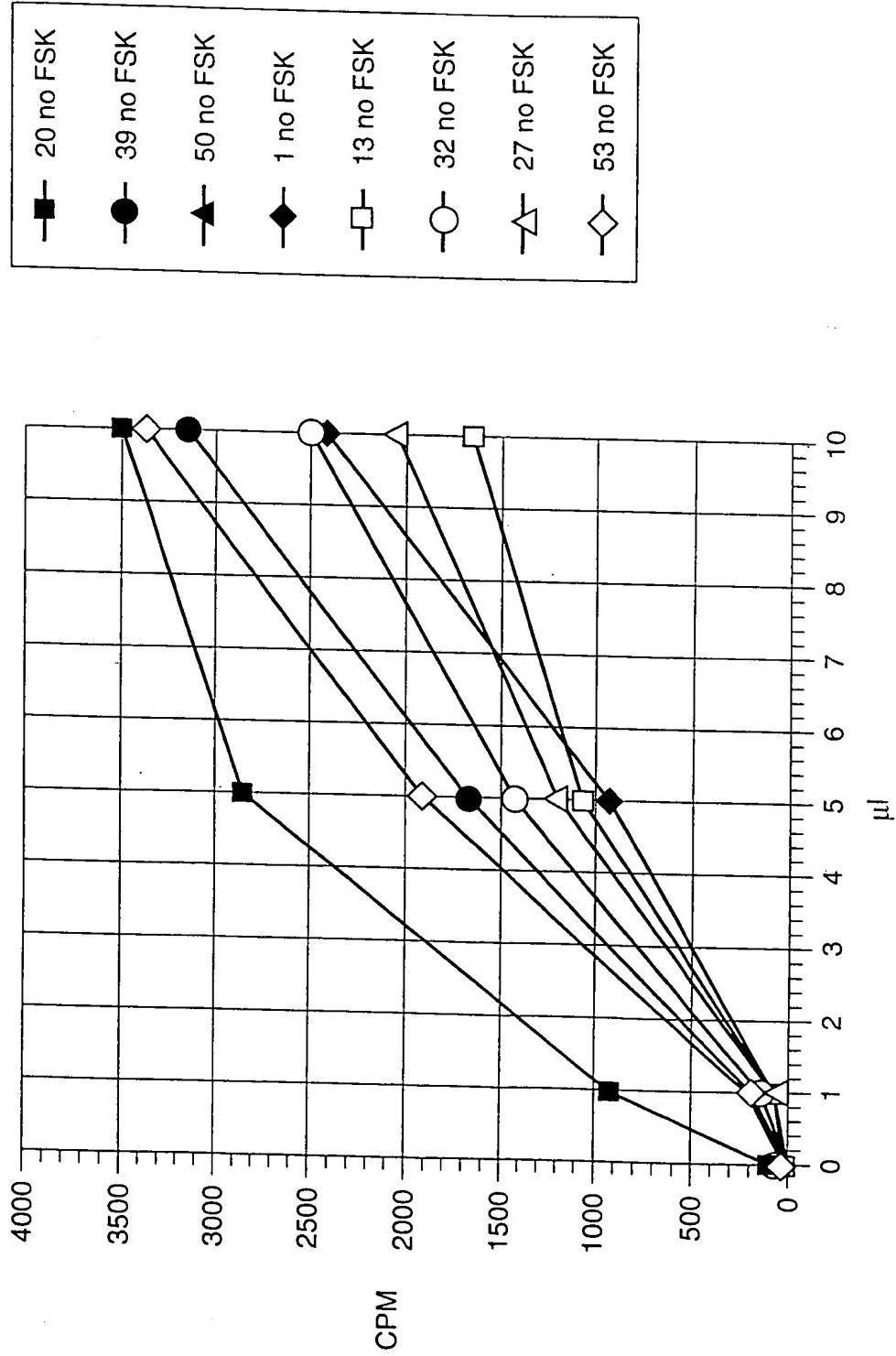
**FIG. 45D**

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBSS5

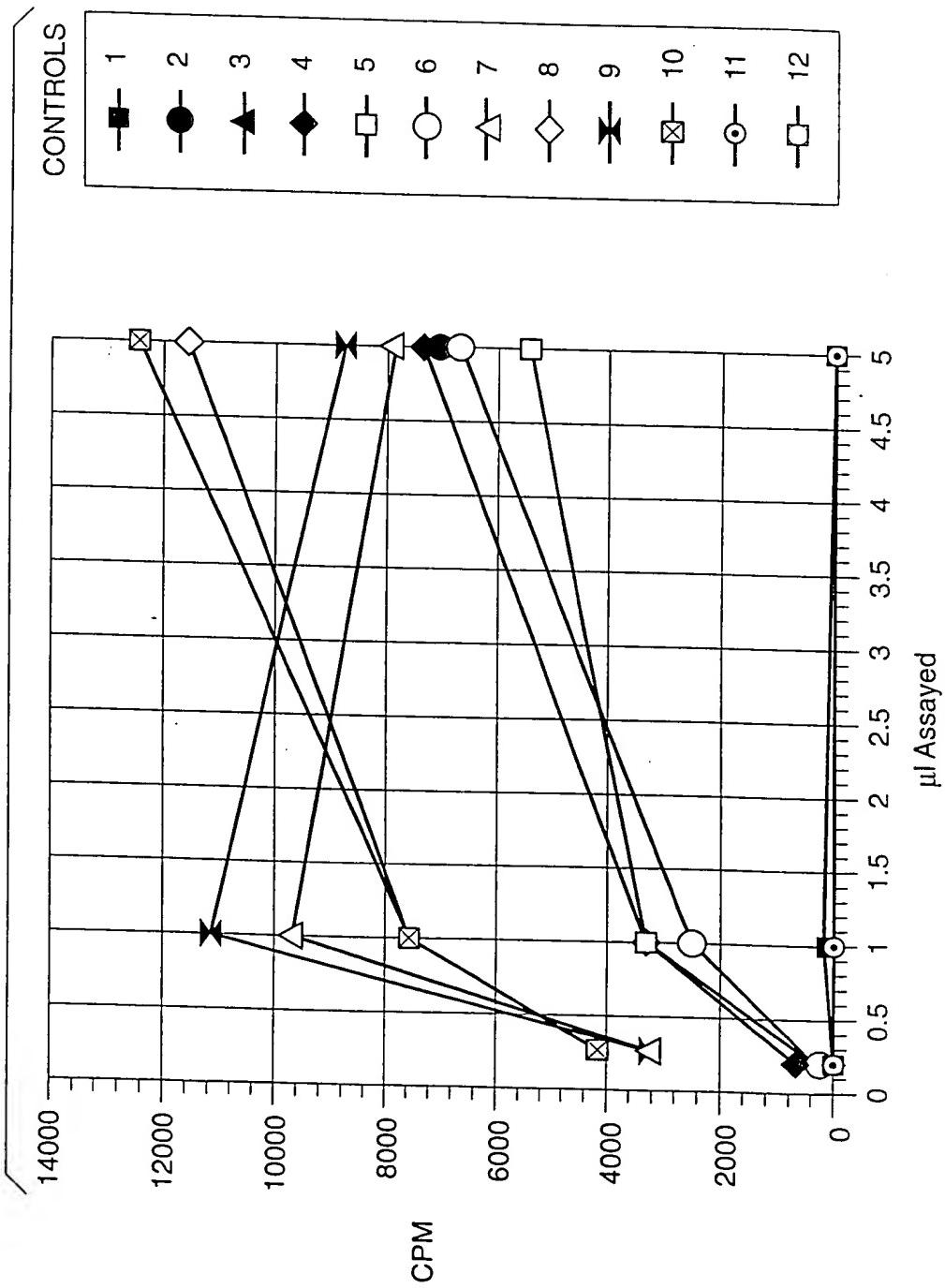
AAA	TGT	GCG	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTC	AAT	GGA	GGG	GAG	TGC	1395
Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	
TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAC	CCC	TCG	AGA	TAC	TTG	TGC	AAG	TGC	1443
Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Tyr	Leu	Cys	Lys	Cys
CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGG	CAA	AAC	TAC	GTA	ATG	GCC	AGC	1491
Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	
TTC	TAC	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA					1530
Phe	Tyr	Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu				
TAGGAGCATG CTCAGTTGGT GCTGCTTCTCT TGTTGCTGCA TCTCCCCCTCA GATTCCACCT																1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGACTGTGCT CATGAGAACAA																1650
TTAACAAAG CAATTGTATT ACTTCCTCTG TTTCGACTA GTTGGCTCTG AGATACTAAT																1710
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATT CAAAGTCTCA CTTTTATTGA																1770
TAAAAATAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA																1830
AAGGGTGTG CTAAGCTGTAA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTGGATT																1890
CAGATGTGT TATTGTGTCAC AAATAAACAT AATAAAAGGA AAAA AAAAAA AAA																1950
																2003

**FIG. 46**  
Schwann Cell Proliferation Assay



**FIG. 47**

**FIG. 48**  
Schwann Cell Assay/Baculovirus Clones



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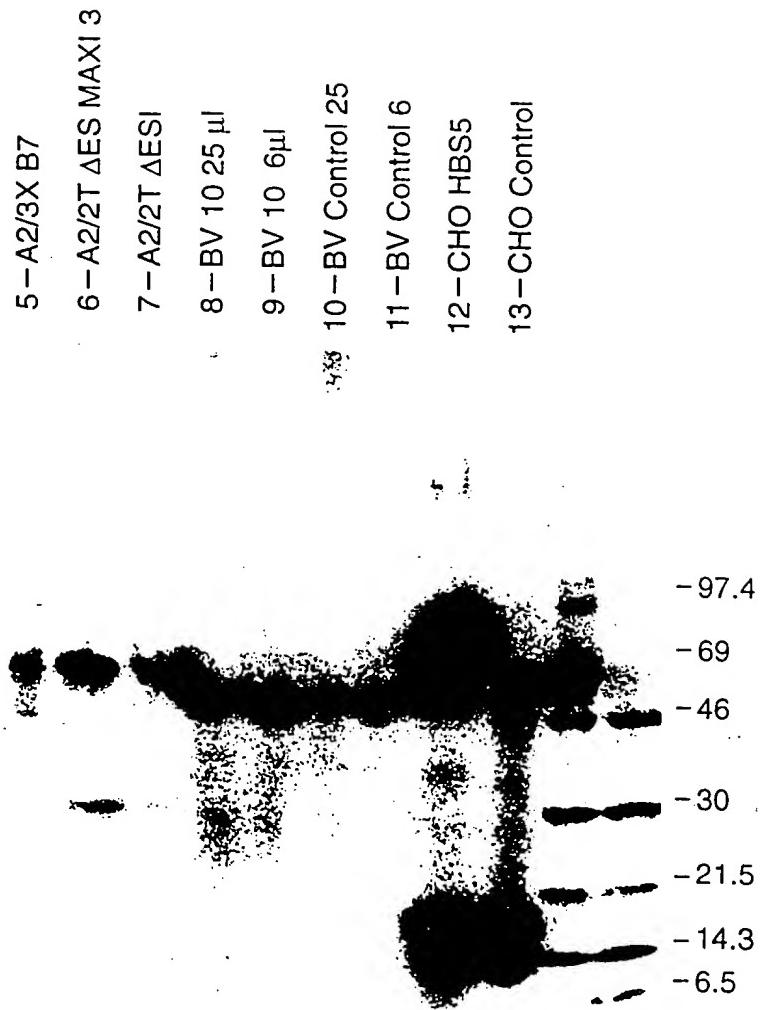
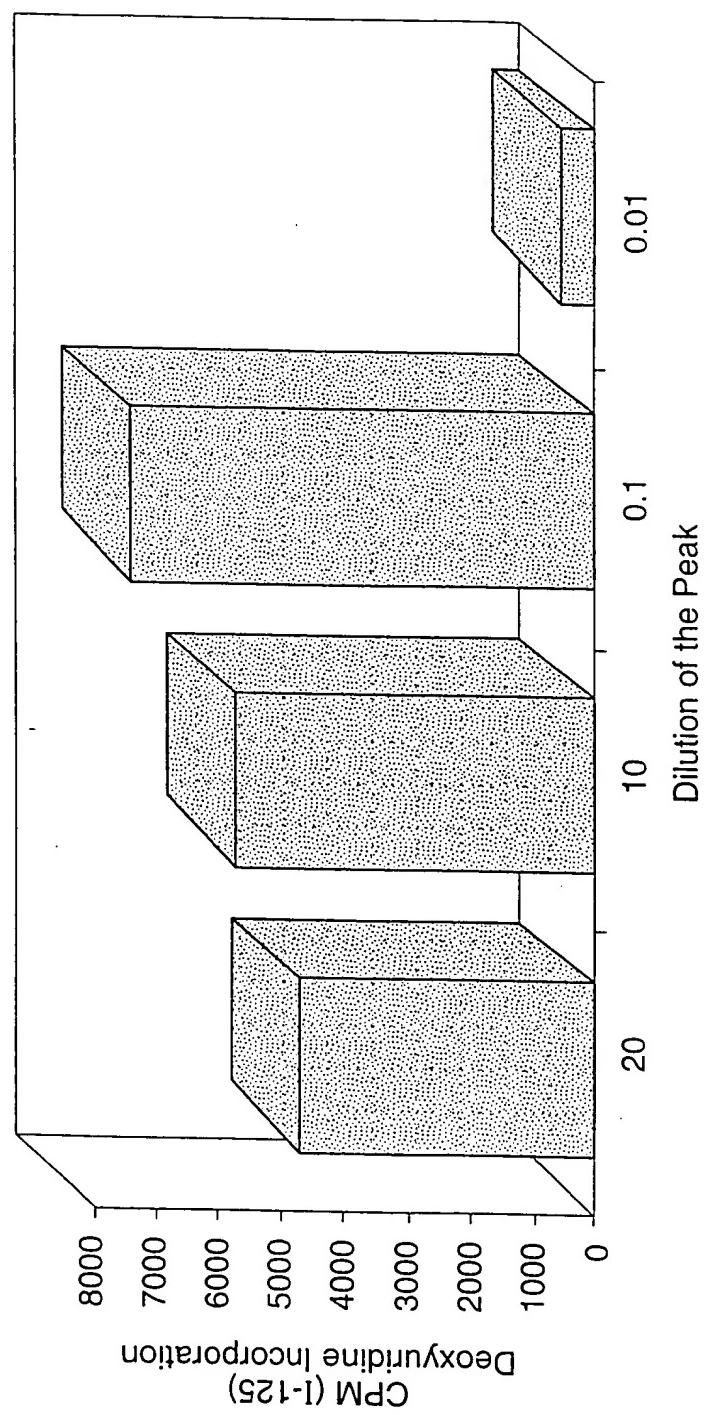
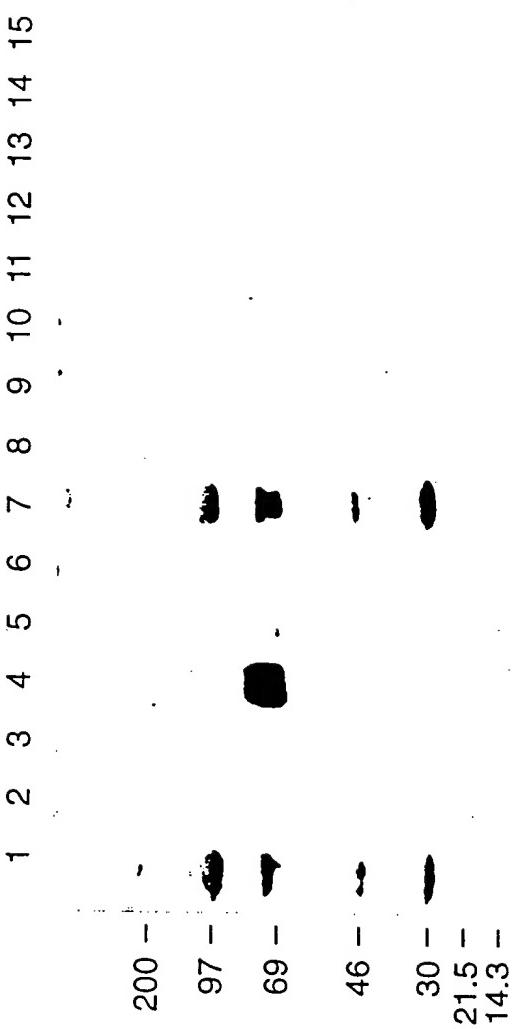


FIG. 49

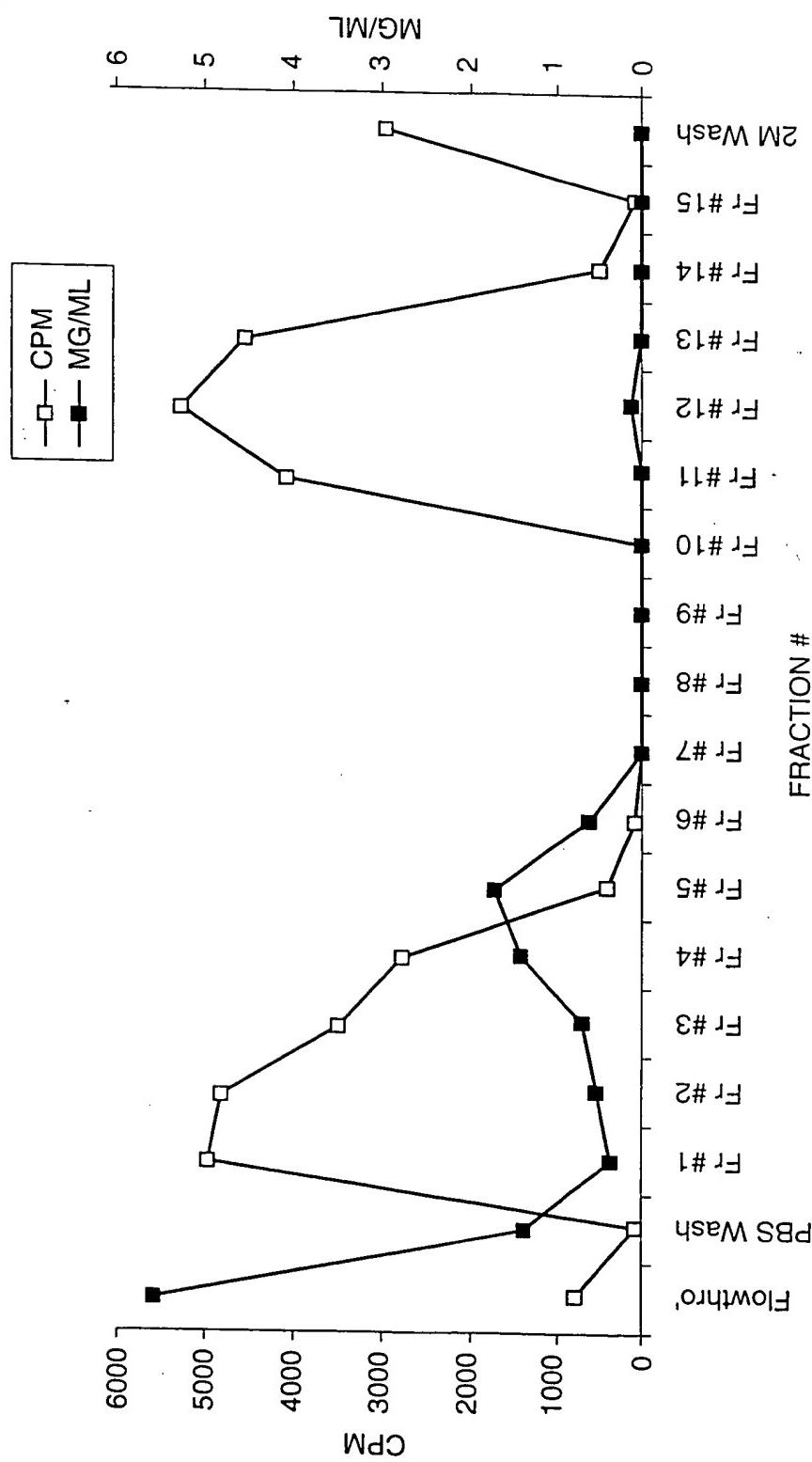
FIG. 50A



**FIG. 50B**

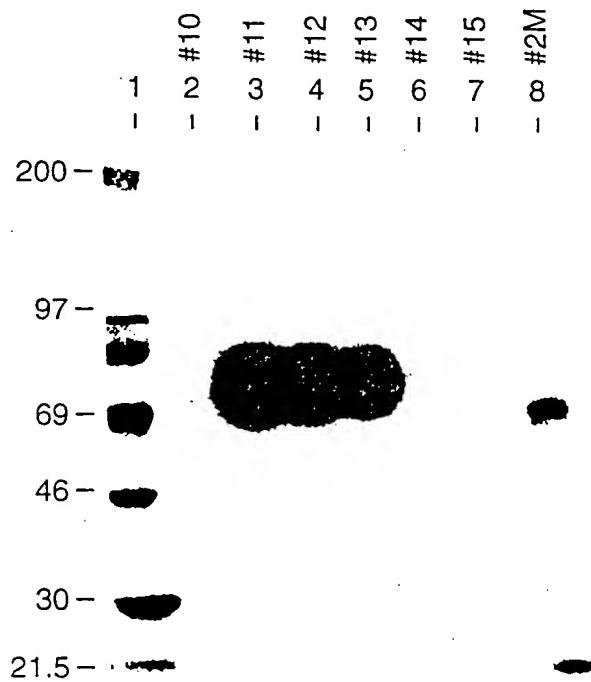
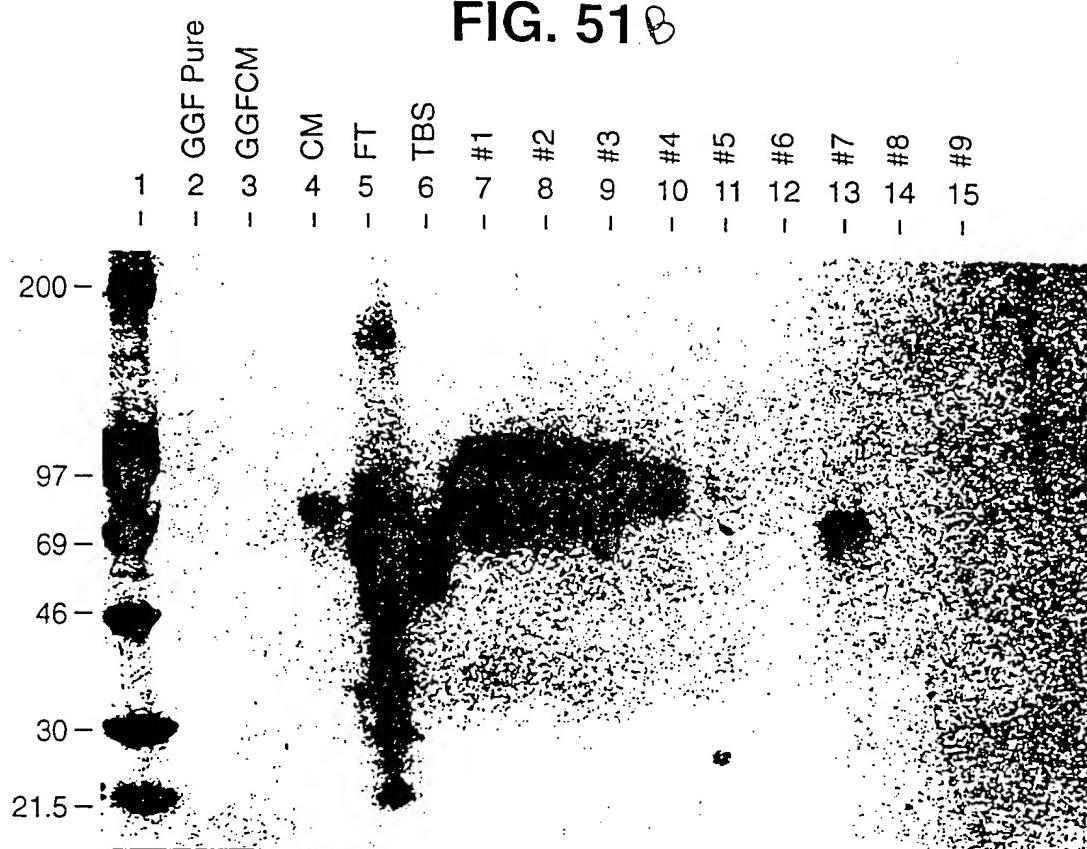


**FIG. 51 A**  
rGGF Purification on Cation Exchange Column



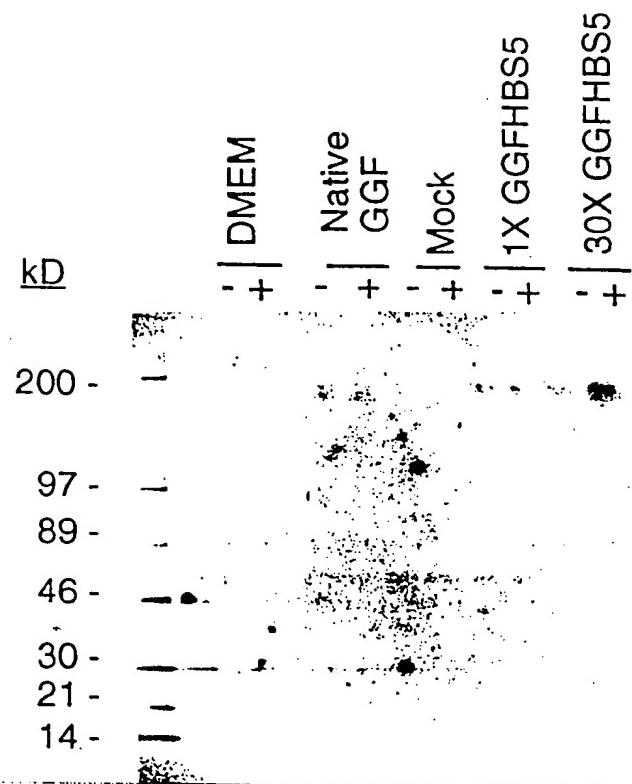
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FIG. 51<sup>B</sup>



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## FIG. 52



SEQ ID NO: 170	GGFHBS5	1	MMRRAPRSGRPGRPRAQRPGSAARSSPPLPLLILLGTAALAPGAAAGNEAAPAGAS	
		II-8	VCYSSPPSVGSVQELAQRAAVVIEGKVHQPQRQQGALDRKAAAAGEAGAWGGDREPPAA	II-4
61	O		O	
121	GPRALGPPAEEPLLAAANGTVPSWPTAPVPSAGEPGEAEAPYLVKVHQVWAVKAGGLRKDSL	II-3		II-1
181	LTVRLGTWGHPAFPSCGRLKEDSRYIFFMEMPDANSTSRAPAAFRASFPPLTGRNLKKEV	II-2	O	II-10
SEQ ID NO: 171	GGFHFB1	241	SRVLCKRC	ALPPQLKEMKSQESAAGSK
SEQ ID NO: 172	GGFBPP5	1	O OM SERKEGRGKGKKKERGSGKKPE SAAGSQSP	R
SEQ ID NO:		R K G D VP GP R	V	
		II-6 II-18	II-14	II-11 I-7, II-12,
268	LVLRCETSSSEYSSLRFKNFKNGNENRKNKPQNQIKIQKKPKSELINKASLADSGEYMC	*		II-13
53				
53		K S S	R	
4	II-1.2	5	S	
328	KVISKLGNDSASANTIVESN	IIITGM PASTEGAVSSESPIRISVSTE GANTSSS	T	ATSTS
113				
113				
6	II-15	8	-	-
354	TTGTSHLVKAEEKEKTFCVNGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYST	*	*	▼
173	A			
173				
9	STPFSLSLPE*			
413				
232				
232				

## FIG. 53

Deduced Sequences  
of Human & Bovine  
Glia Growth Factors

**FIG. 54**